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orein - protei	OM protein - protein search, using sw model	February 3, 2004, 07:43:37; Search time 13.5644 Seconds (without alignments) 1545.568 Million cell updates/sec	US-09-911-777-1 1116 1 MDDSTEREGSRLTSCLKKREENAQISLDGDVTFFGALKLL 218	
ntein - pr	otein	Febru	US-09 1116 1 MDD	
OM pro Run or Title: Perfectsequen	OM protein - pr	Run on:	Title: Perfect score: Sequence:	

283308 seqs, 96168682 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ript	probable membrane	infected cell prot	14	hypothetical prote		sensor histidine k	histidine kinase (conserved hypothet	hypothetical prote	El protein - human	conserved hypothet	hypothetical prote	protein kinase C (95K golgi antigen	protein_kinase_C (chitin synthase (E	superantigen Mtv -	phosphoprotein pho	conserved hypothet	GGDEF family prote	FKBP12 interacting	tumor necrosis fac	citrate (si)-synth	gene mastermind pr	Superantigen Mtv9	transcriptional re	late competence pr	coatomer complex b	alpha-factor recen
SUMMARIES				===	-#	~	LO.	₹#	ın	₹#	ın	m		DO		ſά	0	~	7	0	~	uo	œ	0	m	7	7	œ	.	œ
SU		S57058	WMBEBH	S76714	C81874	836523	F95076	C97944	G64575	B96834	W1WL35	D81148	T01350	KIRTCE	JH0821	KIMSCE	855520	835303	B44307	F75410	F75583	T47576	S11688	T02390	T13998	826387	AF3237	B30338	B55123	S5622
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d	Query Match	8.2	7.9	7.8	7.6	7.6	7.5	7.5	7.5	7.5	7.5	7.4	7.4	7.4	7.3	7.3	7.3	7.2	7.2	7.1	7.1	7.0	7.0	7.0	7.0	6.9	6.9	6.9	6.9	6.9
	Score	91	88	87.5	85	84.5	84	84	83.5	83.5	83.5	83	82.5	82.5	82	81.5	81.5	80.5	80.5	79.5	179	78.5		78	78	77.5	77.5	77.5	77.5	77
	Result No.		7	m	4.	'n	9	7	00	9	10	11	12	13	14	15	16	17	18	19	20	21		23	24	25		27	28	29

73 EKLPAGAKIFEPPAPGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTF 132

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203 YKLEACVCVFE-SKPAKGTKWQRTTNLTFVE--EATVSQVLLKSVTNI-----GHFVF 252

133 VPWLLSFKRGSALYGQVLYTDKTYAMGHLIQRKK 166

||| : | : |: ---KTYFIKHALSSKQ 268

253 TPW-

RESULT 2 WMBEBH infected cell protein ICP18.5 - bovine herpesvirus 2 (strain BMV)

CKON HE CONTRACTOR	procesuase is veau	protein kinase C (mitosis inhibitor	chromosome segrega	protein kinase (EC	probable two-compo	conserved hypothet	hypothetical prote	hypothetical prote	phage-related prot	importin alpha 2 -	carboxylesterase (hypothetical prote			
	E87206	S28942	A25962	AE1947	OKGAR1	D83246	C70302	T19268	T31473	D69946	T30167	871597	876449	T16086	T46458	H86169
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	992	737	877	1208	378	473	592	674	1675	510	531	561	899	1490	278	672
(V	6.9	6.9	6.9	9.9	9	6.8	6.8	6.8	6.8	6.8	6.8	6.8	8.9	6.7	6.7
ī	11	76.5	76.5	76.5	92	16	94	. 92	92	75.5	75.5	75.5	75.5	75.5	75	75
ć	30	31	32	33	34	35	36	. 37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 S57058 Probable membrane protein YJR019w - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein J1614 C;Species: Saccharomyces cerevisiae C;Species: Saccharomyces cerevisiae C;Species: Saccharomyces cerevision 08-Sep-1995 #text_change 19-Apr-2002 C;Accession: S57058; S63780 R;Huang, M.E.; Chuat, J.C.; Galibert, F. A;Reference number: S57052 A;Reference number: S57052 A;Reference number: S57052 A;Reference number: S57052 A;Reference number: S57058 A;Molecule type: DNA A;Residues: 1-1121 <amn> A;Residues: 1-1121 <amn> A;Cross-references: EMBL:Z49538; NID:g1015687; PID:g1015689; MIPS:YJR039w K;Anung, M.E.; Chuat, J.C.; Galibert, F.</amn></amn>
A;Title: Analysis of a 42.5 kb DNA sequence of chromosome X reveals three tRNA genes and
A;Reference number: S63757; MUID:95397595; PMID:7668047 A;Accession: S63780 A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DMA A;Reaidues: 1-1121 < HUA>
A;Cross-references: EMBL:LJ6344 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996 C;Genetics: A;Cross-references: SGD:S0003800
A;Map position: 10R A;Note: YJR039w C;Superfamily: Saccharomyces cerevisiae probable membrane protein YJR039w C;Keywords: transmembrane protein
Query Match 8.2%; Score 91; DB 2; Length 1121; Best Local Similarity 25.3%; Pred. No. 4; Matches 39; Conservative 22; Mismatches 51; Indels 42; Gaps 8;
Qy 15 CLKKREEMKLKECVSILPRKESPSVLLSCCLTVVSFYQVAALQGDLASLRABLQGHHA 72

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hypotherical protein NWA1086 [imported] - Neisseria meningitidis (strain 22491 serogroup C; Species: Neisseria meningitidis (C; Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 (C; Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 (C; Date: 051874; Date: 051874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84349.1; PID:g737978
A;Experimental source: serogroup A, strain Z2491
               -ALPWLLAPNLKSALVFGREDSGLTNEELNQAHRFVRIPVHPQYPSL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 K--TYAMGHLIQRKKVHVFGDELSLVTLFRCIQNLEEGDELQLAIPRENAQISLDGDVTF 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 REEMKLKECVSILPRKESPSVLLSCCLTVVSFYQVAALQGDLASLRAELQGHHAEKLPAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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R;Delius, H.: Hofmann, B.
Bubmitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52;
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                                                                                                                                                                                                            134 NLSQAVMVCTYELYQASLAMETNNQVPGDRLEDGSTMPLA---TNAQL 178
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C.Date: 09-Dec-1993 #sequence_revision 26-Jul-1996 #text_change
                                                                                                                     -NLEEGDELQLAIPRENAQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 213;
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29.6%; Pred. No. 8.2;
ve. 16; Mismatches
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Best Local Similarity 22.9%
Matches 43; Conservative
                                                                                                                175 SL----VTLFRCIQ-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Status: preliminary
A Molecule type: DNA
A; Residues: 1-213 <PAR>
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Best Local Similarity
Matches 45; Conserv
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A; Residues: 1-637 <DEL>
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                    88
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Cippencies: Synchocytis sp.

Alvariety: PCC 6803

Alvariety: PCC 6803

Cipate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000

Cipate: 10-Sep-1999 #text_change 16-Ju
C;Speciee: bovine herpesvirus 2
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Nov-1996
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Nov-1996
C;Accession: B2924.
A;Title: Conservation of a gene cluster including glycoprotein B in bovine herpesvirus the A;Reference number: A94381; MVID:88306231; PMID:2841793
A;Accession: B2924.
A;Accession: B2924.
A;Accession: B2924.
A;Accession: B2924.
A;Accession: B2924.
C;Accession: B2
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A;Status: nucleic acid sequence not shown; translation not shown
A;Residues: 11-240 **CKAN>
A;Residues: 11-240 **CKAN>
A;Cross-references: EMBL:D64004; GB:AB001339; NID:91001701; PID:91208490
A;Cross-references: EMBL:D64004; GB:AB001339; NID:91001701; PID:91208490
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
C;Superfamily: conserved hypothetical protein MTH1849
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C;Species: Synechocystis en
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Matches 46; Conservative
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Best Local Similarity
Matches 52; Conserv
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DKLEYEI---NENVAFD 454
                                            7.5%;
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C;Keywords: phosphotransferase
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                                            Query Match
Best Local Similarity
Matches 47; Conserv
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Matches 56; Conserv
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A; Residues: 1-360 <TOM>
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A;Start codon: GTG
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R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
(Science 293, 496-506, 2001
A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A; Reference number: A55000; MulD:21357209; PMID:11463916
A; Ratus: P55076
A; Residues: 1-563 < KUR>
A; Residues: 1-563 < KUR>
A; Residues: 1-563 < KUR>
A; Cross-references: GB:AE005672; PIDN:AAK74807.1; PID:g14972135; GSPDB:GN00164; TIGR:SP4
C; Genetics:
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R; Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Is, R; Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Is, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, B.J.; Lu, J.; Matsushima, P.; McAhren, S.; Is, P.; Sun, P.M.; Winkler, N.E.
J. Bacceriol. 183, 5709-5717, 2001
A,Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A,Atitle; Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A,Reference number: A97872; MUID:21429245; PMID:11544234
A,Accession: C97944
                                                                                                                                                                                                                                                                          sensor histidine kinase, probable [imported] - Streptococcus pneumoniae (strain TICR4) C;Species: Streptococcus pneumoniae C;Date: 03-Aug_2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
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                                                                122 AKRRLFELPDSGYGNSEVEIQQIQQVEG-HDTVEQ-CSMGSGDSITSSSDERHDETPTRD 179
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                      AK - - I FEPPAPGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADS
                                                                                                              125 ---IOKGSYTFVPWLLSFKRGSALYGQVLYTD 153
                                                                                                                                                             180 IIQILKCSNANAAMLAKFKE---LFG-ISFTE 207
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A.Molecule type: DNA
A.Molecule type: DNA
A.Rosidues: 1-563 «KUR>
A.Cross-reference»
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Conserved hypothetical protein HP0447 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Spacession: G64575
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.A.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Authors: Mallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Reference number: A64520; MUID:97394467; PMID:9252185
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C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C.Accession: B96834
R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDIINWAEF-HDSQRVVQVTKSLATYFRLALNQGKDLICLSDEINHVRQYLFIQKQRYG 440
                                                                                                                                                                                                                                 HHAEKLPAGAKIFEPPAPGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                            323 LRÁKEVGÁ-YELREVTROFNAMLDÓIDOLMVÁIRSQÉETTROYOLÓALSSOINPHFLYNT 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 YTFVPWLLSFKRGSALYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNLEEG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEDESQDAQDEIEKALKDSMFKKLKERAQKLKELDGK----ECFITLNMQYGMHPLLGEL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 -PEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALYGQVLYTDKTYAMGHLIQ 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 ESEITAIKECLDLFMKDE-PDFTFGVITF-----FSEQKRLLEGAL---KGYAN---LE 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                     14 SCLKKREEMKLKECVSILPRKESPSVLLSCCLTVVSFYQVAALQGDLASLRAEL----QG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVLLSCCLTVVSFYQVAALQGDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 RKKVHVF-GDELSLVTLFRCIQNLEEG-----DELQLAIPRENAQISLDGD 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SLRAELOGHHAEKLP--AGAKIFEPPAPGEGNSSONSRNKRAVOG-
                                                                                       10;
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Length
                                                                                  35; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.5%; Score 83.5; DB 2;
24.0%; Pred. No. 5.1;
ive 28; Mismatches 106;
7
DB 2
Score 84;
Pred. No.
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Rifettellin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Science 287, 1809-1815, 2000
A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve-A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
A; Reference number: A81000; MUID:20175755; PMID:10710307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE002439; GB:AE002098; NID:g7226100; PIDN:AAF41279.1; PID:g722610
A;Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                     conserved hypothetical protein NMB0868 [imported] - Neisseria meningitidis (strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 K--TYAMGHLIQRKKVHVPGDELSLVTLFRCIQNLEEGDELQLAIPRENAQISLDGDVTF 211
                                                                                                                                                                                                                                                                                                                                                        C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: D81148
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C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 14-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 SEQVPARGVAVINHPNPLQGGTNTNKVIQTAAKALSKLGFHCYLPNLRGVGGSGGTHDYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 --VTQDCLQLI----ADSETPTIQKGSYTFVPWLLSFKRGS-----ALYGQVL--YTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 RGETÓDCLAVIDYARAQHPEAPEFALSGFSFGGYVATFAAQARTPDLLLLIGAAVCHÝTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---RNKRAVQGPEET----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52;
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A;Cross-references: EMBL:AF069299; NID:g3193311; PID:g3193318
A;Experimental source: cultivar Columbia
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                                                                 125 ---IQKGSYTFVPWLLSFKRGSALYGQVLYTD 153
                                                                                                        ΩB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.4%; Score ou,
23.4%; Pred. No. 3;
Five 29; Mismatches
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R;Ryan, E.; Edwards, J.; Pape, K.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of A. thaliana F6N15.
A;Reference number: Z14297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.4%; Score 82.5; DE 25.1%; Pred. No. 3.6; tive 23; Mismatches
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A;Status: translated from GB/EMBL/DDBJ
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Best Local Similarity 23.4%
Matches 44; Conservative
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FHGKLIVL 199
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A, Note: F6N15.4
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ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

Nature 408, 816-820, 2000

C.A.; Li, J. Gentins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Ttle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: B96834
A;Scatus: preliminary
A;Accession: B96834
A;Scatus: preliminary
A;Molecule type: DNA
A;Residues: 1-596 <STO>
A;Cross-references: GB:AE005173; NID:g6751702; PIDN:AAF27684.1; GSPDB:GN00141
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C;Species: human papillomavirus type 35
A;Note: host Homo sapiens (man)
A;Note: host Homo sapiens (man)
C;Darcession: A40824
B;Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A;Reference number: A40824; MUD:92124753; PMID:1310198
A;Reference number: A40824; MUD:92124753; PMID:1310198
A;Reference number: A40824
A;Status: translation not shown
A;Status: translation not shown
A;Residues: 1-630 <AMR>
A;Residues: 1-630 <AMR>
A;Residues: 1-630 <AMR>
C;Superfamily: papillomavirus El protein
C;Keywords: early protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSAGTKSDQEEDDLEDGFSELEGSKSGQGSTSSDEDEGKLSADBEEBEBLDLIE--TDVS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 TPTIQKGSYTFVPWLLS---FKRGSALYGQVLYTDKTYAMGH------LIQRKKVH 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 VFG-------DELSLVTLFRCIQNLEEGDELQLAIPRENAQISLDGD 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AK--IFEPPAPGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADS------ETPT-- 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 19.3%;
Matches 47; Conservative 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLY 232
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Best Local Si
Matches 45,
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Gaps

		Db 382 TDGQLASPGENGEVRQGQAKRLGLDEPNFIKVLGKGSFGKVMLAELKGKDEVYAVKVL 439
à	18 KREEMKLKECVSILPRKESPSVLLSCCLTVVSF-YQVAALQGDLASLRAELQGHHAEKLP 76	Qy 164 RKKVHVFGDELSLVTLFRCIQNLEEGDELQLAIP 197
<u>-</u>	70 KRPDAVVSICFEAQARLRDPIYGCVSHIVSLQQQVVSLQTELSYLQAHL 118	: : : 440 KKDVILODDOVDCTMTEKRILALARKHP
ờ	77 AGAKIFEPPAPGEGNSSONSRNKRAVQSPEETVTQDCLQLIADSETPTIQKGSYTFVPWL 136	
q ₀	:: :	198 R
ò	137 LSFKRGSALYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNLEBGDELQLAI 196	DD 500 R 500
q		RESULT 14
ò	197 PRE 199	JH0821 95K golgi antigen - human
QQ	200 ARE 202	C;Species: Homo sapiens (man) C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000
	60	
protein C.Specie	kinase C (EC 2.7.1) epsilon - rat	A;Title: Molecular characterization of two human autoantigens: unique cunas encoding 95- A;Reference number: JH0820; MUID:93301617; PMID:8315394
	29-1992 #sequence revision 30-Sep-1992 #text_change 11-Jun- B28163; B26408; \$00216	A;Molecule type: mRNA A;Residues: 1-620 <fri></fri>
R,Ono, Y J. Biol.	K.; Nishizuka, Y.	A;Cross-references: EMBL:L06147; NID:g306781; PIDN:AAA35920.1; PID:g306782 A;Experimental source: hepatic carcinoma AT CC HB8065 cell line
A, Title A, Refere	: The structure, expression, and properties of additional members of the protein ence number: A92717; WUID:88198270; PMID:2834397	A; Note: this protein has alpha-helical structure with absence of beta-sheets
A; Accest A; Molect	A,Accession: B28163 A,Molecule type: DNA	
A: Cross	168: 1-737 <ono> references: GB:M18331: NTD:G206182: PIDN:AAA41872.1: PID:G206183</ono>	vative 20; Mismato
(R; House)	(G.M.; O'Brian, C.A.; Johnson, M.D.; Kirschmeier, P.; Weinstein, I.B.	LISC
A, Title	i Isolation of CDNA clones encoding protein kinase C: evidence for a protein kina	Db 317 DGLDREEEEDEBEEEEERAVPQPMPSIPEDLESREAMVAFFNSAVASAEEEQ 369
A; Acces	1201. 1820.01. 17.11.17. 17.11.17.17.17.17.17.17.17.17.17.17.17.1	LQGHHA
A; Residu	115 - Lype: MINAN 106: 397-447, GORGLHDDREEDFGSGAET', 467, 'LSNPTLLLLEPDGGPPLLRQ', 487-545,'C',547-636 Treferences: CR-NT-573: NID2766192. DTNN.33441877 1. DID2766193	Db 370 ARIRGQLKEQRVRCRRLAHLLASAQKEPEAAAPAPGTGGDSVCGETHRALQGAMEK 425
C, Commer	it: Protein kinase C epsilon and epsilon, appear to be encoded by the same gene a	Cy 106
A;Descri	tour: sption: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin artivity is calcium-independent phospholinid-dependent and activated by diacyl	Db 426 LQSRFMELMQEKADLKERVEELEHRCIQLSGETDTIGEY 464
C; Superi	se C delta: , protein kinase C zimo-binding repeat ho icing; ATP; autophosphorylation; duplication; phorb	RESULT 15
C F,156-16	sphorylation motif	KIMSCE protein kinase C (EC 2.7.1) epsilon - mouse
F;170-2;	F;170-220/Domain: protein kinase C zinc-binding repeat homology <kz1> F;243-292/Domain: protein kinase C zinc-binding repeat homology <kz2></kz2></kz1>	C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text change 21-Nov-1997
F;406-6	inase homology <kin> inase ATP-binding motif</kin>	C;Accession: S02270 R;Schaap, D.; Parker, P.J.; Bristol, A.; Kriz, R.; Knopf, J.
F;170,20	ite: zinc (His, Cys, Cys, Cys) #status predicted ite: zinc (Cys, Cys, His, Cys) #status predicted	FEBS Lett. 243, 351-357, 1989 A,Title: Unique substrate specificity and regulatory properties of PKC-epsilon: a ration
F; 256, 259,	<pre>ite: zinc (His, Cys, Cys, Cys) #status predicted ite: zinc (Cys, Cys, His, Cys) #status predicted</pre>	
,703,7	oo,534,634/Accive site: 178, Giu, ABP, 178 #Status predicted 10/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred	Ajstatus: nucleic acid sequence not snown; not compared with conceptual translation Ajsolecule type: mRNA * notice type: mRNA
Query Best I	Query Match 7.4%; Score 82.5; DB 1; Length 737; Best Local Similarity 20.7%; Pred. No. 15;	A; Residues: 1-/3/ <sch> C; Function: A; Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin</sch>
Match	; Conservative 34; Mismatches 88; Indels 69; Gaps 10;	A;Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl C;Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology; pr
ò	76	C;Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipid b F;156-161/Region: pseudophosphorylation motif
q _Q	DARGIAKVLADLGVTPDKITNSGQRRKKLA 324	F;170-220/Domain: protein kinase C zinc-binding repeat homology <kz1> F;243-292/Domain: protein kinase C zinc-binding repeat homology <kz2></kz2></kz1>
ð í	113	F;416-668/Domain: protein kinase homology <kin> F;414-422/Region: protein kinase ATP-binding motif.</kin>
ga .	EDDRSKSAPTSPCDQELKELENNIRKALSFDNRGEEHRASSS 381	F;170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted F;183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
à	114 LQLIADSETPTIQKGSYTFVPWLLSFKRGSALYGQVLYTDKTYAMGHLIQ 163	F;243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted F;256,259,281,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted

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F;437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted
F;703,710/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred
                                                                                                                                                                                                                                       Query Match 7.3%; Score 81.5; DB 1; Length 737; Best Local Similarity 20.7%; Pred. No. 19; Matches 50; Conservative 33; Mismatches 89; Indels 69; Gaps 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          382 TDGQLASPGENGEVRPGQAKRLGLDBFNFIKVLGKGSFGKVMLAELKGKDEVYAV--KVL 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 REEMKLKECVSILPRKESPSVLLSCCLTVVSFYQVAALQGDLASLRAEL--QGHHAEKLP 76
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Listing first 45 summaries
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KAPR_APLCA	B3A2_CAVPO	YQBA BACSU	IMA2 CAEEL	ESTA_DROPE	TNFA DELLE	TSH DROME	SPA1 HUMAN	ABC2 HUMAN	PR7R_MMTVG	PR7L MMTVG	YSO1_CAEEL
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	ALIGNMENTS
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a S	T138 HUMAN STANDARD; PRT; 285 AA. Q9Y275;
텀	2001 (Rel. 40, Creat
4 5	
D E	or ligand superfamily membe xpressed ligand 1) (TALL-1)
88	-activating
g e	derived TNF-like molecule). TNFSF13B OR TALL1 OR BLYS OR BAFF OR ZTNF4.
So	Homo sapiens (Human).
88	kukaryota; Metazoa; Chordata; Craniata; Vertebrata; kuteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
X N	NCBI_TaxID=9606;
RP.	SEQUENCE FROM N.A.
X 6	MEDLINE=99260341; PubMed=10331498;
몺	"TALL-1 is a novel member of the TNF family that is down-regulated by
RT	ogens."
Z Z	 Leukoc. Bioi. 65:680-683(1999). [2]
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 134-148.
ž :	MEDLINE=99288033; PubMed=10359578;
¥ &	Schielder F., Mackay F., Stellier V., Holimaini N., Boumer CL., Holler N. Ambrose C. Lawton P. Bixler S. Acha-Orbes H.
2	D., Romero P., Werner-Favre C., Zubler R.H., Bro
RA Ta	Techopp J.;
RT	י ל די וווידי
RL	J. Exp. Med. 189:1747-1756 (1999).
RN	[3]
ጸ 6 ር	SEQUENCE FROM N.A.
2 2	IISSUE-MONOCYTES, and Neutrophiris, MEDLINE=99329343; Pubmed=10398604;
R.	Feng P
RA 6	Soppet D., Charters M., Gentz R., Parmelee D., Li Y., Galperina O.,
5 5	S.M., Olsen H.S., Fikes
RT	"BLyS: member of the tumor necrosis factor family and B lymphocyte
R.	stimulator.";
R. R.	Science 285:260-263(1999). [4]
RP.	
RA!	., Piddington C., O'Hara P.;
R	"Homo sapiens homolog of tumor necrosis factor.";
2 2	to the EMBL/Genbank/DDBJ
RP	SEQUENCE FROM N.A.
2 5	TISSUE=Dendritic cell;
¥ £	Many w., wan i., iu i., cao A.; "A novel dendritic cell-derived TNF-like molecule.":
R.	Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
RN	[6]

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**XEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins P.S., Wagner L., Sheafer C.F., Bhat N.K., A Altschul S.F., Zeeberg B., Butcow K.H., Scheefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheez T.E., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheez T.E., A Stapleton M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Maruy D.M., Sodergren E.J., Lu X., Gibbs R.A., A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Miting M., Madan A., Young A.C., Shevchenko Y., Gibbs R.A., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Generation and initial analysis of more than 15,000 full-length Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M., McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M., Boyle W.J., Sarosi I., Hau H., Senaldi G., Theill L.E., "APRIL and TALL-I and receptors BCWA and TACI: system for regulating
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MEDLINE-21686304; PubMed=11827482;
Karpusa M., Cachero T.G., Qian F., Boriack-Sjodin A., Mullen C.,
Strauch K., Hau Y.-M., Kalled S.L.;
"Crystal structure of extracellular human BAFF, a TNF family member that stimulates B lymphocytes.";
That stimulates B lymphocytes.";
J. Mol. Biol. 315:1145-1154(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 142-285.
MEDLINE=21842897; PubMed=11853672;
Liu Y., Xu L., Opalka N., Kappler J., Shu H.-B., Zhang G.;
"Crystal structure of sTALL-1 reveals a virus-like assembly of TNF family ligands.";
cell 108:383-394 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-135 FROM N.A., AND VARIANT THR-105.

Wheasaki A., Tsukorchiya N., Fukazawa T., Hashimoto H., Tokunaga K.,
"New polymorphisms of human BLyS gene.",
"Demirted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                     MEMBER 13B, MEMBRANE FORM.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
MEMBER 13B, SOLUBLE FORM.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                          TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .). (HIGH MANNOSE).
                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Signal-anchor; 3D-structure;
                                                                                                                                                                                                                                                                                        MIN; 603969; -.
GO; GO:0005625; C:soluble fraction; TAS.
GO; GO:000283; P:cell proliferation; TAS.
GO; GO:000284; P:positive regulation of cell proliferation; TAS.
GO; GO:0007165; P:gignal transduction; TAS.
InterPro; IPR066052; TNP_family.
PRART; SM00207; TNF, 1.
PROSITE; PS00251; TNF, 1.
PROSITE; PS50049; TNF_1: FALSE_NEG.
INDUCTION: UPREGULATED BY EXPOSURE TO INTERFERON-GAMMA. DOY
REGULATED BY PHORBOL MYRISTATE ACETATE/IONOMYCIN TREATMENT
PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
                                          PTM: N-glycosylated. SIMILARITY: Belongs to the tumor necrosis factor family.
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CLEAVAGE.
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/FTId=VAR_013483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL)
                                                                                                                                                             EMBL, AF136293, AAD29421.1; --
EMBL, AF116456, AAD25356.1; --
EMBL, AF122600, AAD21092.1; --
EMBL, AF134715, AAF01432.1; --
EMBL, AF134715, AAF6019.1; --
EMBL, AB073225, BAB90856.1; --
EMBL, AB073225, AAH20674.1; --
                                                                                                                                                                                                       EMBL; AF134715; AAF60219.1; --
EMBL; AB070225; BAB90856.1; --
EMBL; BC020674; AAH20674.1; --
PDB; IKXG; 03-APR-02.
PDB; IKD7; 12-NOV-02.
GGDB*, HGNC; 11929; TNFSF13B.
MIM; 603969;
                               PROTEOLYTIC PROCESSING.
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MW; 48ED0D7AB38C8867 CRC64;

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                                                                                                                        61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
                                                                                                                                                GEGNSSONSRNKRAVOGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL-- 145
                                                                                                                                                                          GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
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                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Tumor necrosis factor ligand superfamily member 13B (B cell-activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Polymorphism and chromosomal mapping of the mouse gene for B-cell activating factor belonging to the tumor necrosis factor family (Baff) and association with the autoimmune phenotype."; Immunogenetics 53:810-813(2001).

-!- FUNCTION: Cytokine that binds to TNPRSF13B/TACI and TNFRSF17/BCMA. TNFSF13/APRIL binds to the same 2 receptors. Together, they form a 2 ligands -2 receptors pathway involved in the stimulation of B-and T-cell function and the regulation of humoral immunity. A third B-cell specific BAFF-receptor (BAFFR/BR3) promotes the survival of mature B-cells and the B-cell response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "BAFF, a novel ligand of the tumor necrosis factor family, stimulates B cell growth.";
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                          Gaps
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Holler N., Ambrose C., Lawton P., Bixler S., Acha-Orbea H.,
Valmori D., Romero P., Werner-Favre C., Zubler R.H., Browning J.L.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21850530; PubMed=11862414;
Jiang Y., Ohtsuji M., Abe M., Li N., Xiu Y., Wen X.S., Shirai T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS
                       67;
DB 1; Length 285;
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PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
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93.4%; Score 1042.5; 76.5%; Pred. No. 2.9e
                        0; Mismatches
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MEDLINE=99288033; PubMed=10359578;
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                        Conservative
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           Similarity
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TNFSF13B OR BAFF.
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     EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCLTVVSFYQVAALQGDLASLRAELQGHH-----AEKLPAGAKIFEPPAPGEGNSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---VTQDCLQLIADSET
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120 RGHRNRRAFÇGPESTEQDVDLSÁPPAPCLPGCRHSQHDDNGMNLRNIIQDCLQLIADSDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVHVFGDELSLVTLFRCION-------LEEGDELQLAIPRENAQISLDGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEMBER 13B, MEMBRANB FORM.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
MEMBER 13B, SOLUBLE FORM.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MDESAKTLPPPCLCFCSEKGEDMKV-GYDPITPQKEEGAWFGICRDGRLLAATLLLALLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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075888; Q96HV6; Q9PIM8; Q9PIM9;
16-OCT-2001 (Rel. 40, Created)
15-OST-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-OCT-2001 (Rel. 42, Last annotation update)
16-OCT-2001 (Rel. 42, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
116-OCT-2001 (Rel. 40, Last an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46; Indels
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the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 N -> S (IN STRAIN NZB).
34192 MW; F3DE6056E66034B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL) CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 623.5; DB 1
; Pred. No. 5.5e-51;
24; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00207; TNP; 1. —
PROSITE; PS00251; TNF 1; FALSE_NEG.
PROSITE; PS50049; TNF 2; 1.
                                                                                                                                                                                                                                                                                                                       EMBL; AF119383; AAD22475.1; -.
EMBL; AF352245; AAL83939.1; -.
MGD; MGI:1344376; Tnf8f13b.
InterPro; IRROGOS2; TNF_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytokine; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 ONSRNKRAVOGPEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIFFGALKLL 218
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CONFLICT
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Atausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Browner R.F., Jordan H., Moore T., Max S.I., Wang J., Hateh F.,
A Stapleton M., Soares M.B., Bonaldo M.F., Caravinci P., Prange C.,
A Brownstein M.J., Ugdin T.B., Toshiyuki S., Caranici P., Prange C.,
A Brownstein M.J., Ugdin T.B., Toshiyuki S., Caranici P., Prange C.,
A Brownstein M.J., Worley K.C., Hales G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Rading M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield M. Marna Marra M.A.,
Bromeration and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21170294; PubMed=10973284; Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M., McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M., McCabe S., Qiu W.R., Sarosi I., Hsu H., Senaldi G., Theill L.E.; "APRIL and TALL-I and receptors BCMA and TACI: system for regulating humoral immunity.";
                                                                                                                                                                                                                                                                                                                                                                                                       Shu H.-B., Hu W.-H., Johnson H.; "TALL-1 is a novel member of the TNF family that is down-regulated by
                                                                                                                                                                              Hahne M., Kataoka T., Schroeter M., Hofmann K., Irmler M., Bodmer J.-L., Schneider P., Bornand T., Holler N., French L.E., Schata B., Rimoldi D., Tschopp J.; "APRIL, a new ligand of the tumor necrosis factor family, stimulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA AND GAMMA).
MEDLINE-20168636; PubMed=10706119;
Kelly K.A., Manos E.J., Jensen G.T., Nadauld L., Jones D.A.;
Kelly K.A., a tumor necrosis factor-like ligand, stimulates cell
"APRIL/TRD-1, a tumor necrosis factor-like ligand, stimulates cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Farth of the property of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21486098; PubMed=11571266; Lopez-Fraga M., Fernandez R., Albar J.P., Hahne M.; Pernandez R., Albar J.P., Hahne M.; "Biologically active AFRIL is secreted following intracellular processing in the Golgi apparatus by furin convertase."; EMBO Rep. 2:945-951 (2201).
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                                 Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99260341; PubMed=10331498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leukoc. Biol. 65:680-683(1999).
                                                                                                                                                       MEDLINE=98416181; PubMed=9743536;
                                                                                                                                                                                                                                                                               tumor cell growth.";
J. Exp. Med. 188:1185-1190(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cancer Res. 60:1021-1027(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-247 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                      SEQUENCE FROM N.A.
                            Mammalia, Euther
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        mitogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         death.
CC RATER SERVER SER
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. - . N (in isoform Beta).

/FIId=VSP_06450.

Missing (in isoform Gamma).

/FIId=VSP_006451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 LSCCLTVVSFYQVAALQGDLASLRAE---LQGHHAEKLPAGAKIFEPPAPGEG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN TRANSFORMED CELL LINES, CANCERS OF COLON, THYROLD, LYMPHOLD TISSUES AND SPECIFICALLY EXPRESSED IN MONOCYTES AND MACROPHAGES.
INDUCTION: DOWN-REGULATED BY PHORBOL MYRISTATE ACETATE/IONOMYCIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO, GO:0008284; P:positive regulation of cell proliferation; TAS. GO:0007165; P:signal transduction; TAS. InterPro; IPRO60612; TNF_family. PF00229; TNF; 1. SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64; Indels 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKRR->AKRA: ABOLISHES PROTEOLYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: The precursor is cleaved by furin. SIMILARITY: Belongs to the tumor necrosis factor family.
INFRSF17/BCMA. May be implicated in the regulation of tu growth. May be involved in monocyte/macrophage-mediated immunological processes. SUBUNI: Homotrimer (Potential). SUBCELLULAR LOCATION: Secreted. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 13.6%; Score 152; DB 1; Length 250; 1 Similarity 24.9%; Pred. No. 5.8e-07; 58; Conservative 31; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N -> S (IN REF. 5).
F -> L (IN REF. 5).
AE1A6B9457F6E298 CRC64;
                                                                                                                                                                         Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEMBER 13.
CLEAVAGE (BY FURIN)
                                                                                                                                                                                                                                                                                                                                                   IsoId=075888-3; Sequence=VSP_006451;
                                                                                                                                                                                                                                                                                       IsoId=075888-2; Sequence=VSP_006450;
                                                                                                                                                                                                    Name-Alpha;
IsoId=075888-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00251; TNF 1; 1.
PROSITE; PS50049; TNF 2; 1.
Cytokine; Immune response; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROCESSING
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EMBL, AF18629, AAD29422.1; --
EMBL, AF184972; AAF01321.1; --
EMBL, AF114011; AAF59828.1; --
EMBL, AF114012; AAF59829.1; --
EMBL, AF114013, AAF59829.1; --
EMBL, AF114013, AAF59830.1; --
EMBL, BC008042; AAF08042.1; --
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MIM; 604472; -.
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124
                                                                                                                                                                                                                                                                                                                     Name=Gamma;
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MEDLINE=21085660; PubMed=11217851;

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Wynshav-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Buzuki H.,
85 EQSSDALEAWENGERSRKRRAVLTQKQKKQHSVLHLVPINAT-SKDDSDVTEVMWQPALR 143
                                                                                                                                                                   --LYGOVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCI
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Q9D77; Q9ERP1;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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SIMILARITY: Belongs to the tumor necrosis factor family.
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-!+ FUNCTION: Cytokine that binds to TWFRSF13B/TACI and to TYFRSF17N CYA. May be implicated in the regulation of tu growth. May be involved in monocyte/macrophage-mediated
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SUBUNIT: Homotrimer (Potential).
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MEDLINE=21170294; PubMed=10973284;
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  and for commercial
                          (See http://www.isb-sib.ch/announce/
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103 KKKHSVLHLVPVNITSKADSDV-----TEVMMQPVLRRGRGLBAQGDIVRVWDTGIY 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QGDLASLRAE---LQGHHAEKLPAGAKIFE----PPAPGEGNSSQNSRNKRAVQGPEE
                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein.
BY SIMILARITY.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                           EMBL; AF294825; AAG22534.1; -.
BML; AF00514; BAB26332.1; -.
MGD; MGI:191683; TheBE613.
GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
InterPro.; PRO06061; TNR_family.
PF00229; TNF; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS00021; TNF 1.
PROSITE; PS00029; TNF 2: 1.
Cytokine; Immune response; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEMBER 13.
CLEAVAGE (BY FURIN) (BY SIMILARITY).
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.8%; Score 143; DB 1; Length 241; 26.3%; Pred. No. 3.8e-06; cive 23; Mismatches 68; Indels 6
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Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
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4896D03BDBC712A4 CRC64;
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NCBI TaxID=4932;
Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
N-LINKED (GLCNAC.
MISSING (IN REF. 2
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(Rel. 33, Last sequence update)
(Rel. 38, Last annotation update)
  modified and this statement is not removed.
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                          entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 AA; 26889 MW;
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S0003800; YJR039W.
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                                                                                                                                                                                     155 CLEE-TDVKLSYVTS-----SPIVSIDACINFNDF----LDKDVFTLSILTRAHNEVA 202
                                                                                                                                                                                                                              73 EKLPAGAKIFEPPAPGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTF 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALYG--QVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNLEEGDELQLAIPRENA 201
                                                                                                                                             72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probable processing and transport protein (Infected cell protein 18.5) (ICP18.5 protein) (72 kDa protein).
                                                                                                                                                                                                                                                      203 YKLEACVCVFE-SKPAKGTKWQRTTNLTFVE--EATVSQVLLKSVTNI-----GHFVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Conservation of a gene cluster including glycoprotein B in bovine herpessirus type 2 (BHV-2) and herpes simplex virus type 1 (HSV-1).", Virology 165:388-405(1988).
-!- FUNCTION: THIS PROTEIN MAY AFFECT TRANSLOCATION OF THE VIRUS GLYCOPROTEINS TO MEMBRANES. IT IS INVOLVED IN CAPSID MATURATION.
-!- SIMILARITY: BELONGS TO THE HERPESVIRUSES PRIP FAMILY.
PIR; B29242; WMBEBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 CLKKREEMKLKECVSILPRKESPSVLLSCCLTVVSFYQVAALQGDLASLRAELQGHH--A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SILPRKESPSVLLSCC---LTVVSFYQVAALQ-GDLASLRAELQGHHAEKLPAGAKIFEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAPGEGNSSONSRNKRAV-QGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGS
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovine herpesvirus type 2 (strain BMV) (Bovine mammillitis virus).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88306231; PubMed=2841793;
Hammerschmidt W., Conraths F., Mankertz J., Pauli G., Ludwig H.,
                                                                                                    42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68;
                                                          DB 1; Length 1121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.9%; Score 88; DB 1; Length 664; larity 23.5%; Pred. No. 2; Conservative 33; Mismatches 49; Indels
                                                                                                    Indels
                 1121 AA; 127438 MW; 9C512A25E0DA4B7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro, IPR000501; Proc_transpt.
Pfam; PF01366; PRTP; 1.
Late protein; Capsid assembly.
SEQUENCE 664 AA; 72367 MW; A84F7ED8EBE24D29 CRC64;
                                                                                                    51;
                                                                                                                                                                                                                                                                                                               133 VPWLLSFKRGSALYGQVLYTDKTYAMGHLIQRKK·166
                                                                                                                                                                                                                                                                                                                                                      -----kTYFIKHALSSKQ 268
                                           8.2%; Scol.
25.3%; Pred. No. 2;
...e 22; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1990 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 664 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                  39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
Hypothetical protein.
                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                          253 TPW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSVB2
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                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
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PRTP_HSVB2
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                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 IGSYVMTNKPGDFRFILGPLAYAAQSGRWISIBEITTISQDSLLLLSSVVNTRTLSVGSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 LLSCCLTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAKIFEPPAPGEGNSSQNSR--
                                                                                                                                                                                                                                                                                       MEDINE-20189616; PubMed-10930750; Markhur A.G., Morrison H.G., Nixon J.E., Passamaneck N.Q., Kim U., Hinkle G., Crocker M.K., Holder M.E., Farr R., Reich C.I., Olsen G.E. Aley S.B., Adam R.D., Gillin F.D., Sogin M.L.; "The Giardia genome project database."; FEMS Microbiol. Lett. 189:271-273(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION, GENE NAME, AND SIMILARITY WITH OTHER FAMILY MEMBERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=12102729;
Garbarino J.E., Gibbons I.R.;
"Expression and genomic analysis of midasin, a novel and highly conserved AAA protein distantly related to dynein.";
BMC Genomics 3:18-18 (2002).
-!- FUNCTION: May function as a nuclear chaperone and be involve the assembly/disassembly of macromolecular complexes in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
                                                                                                                                                     Giardia lamblia (Giardia intestinalis).
Bukaryota, Diplomonadida, Hexamitidae, Giardiinae, Giardia.
NCBI_TaxID=5741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 4835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3A9E12417DB04A50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- SIMILARITY: Contains 1 VWFA domain.
-i- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 87; DB 1;
; Pred. No. 31;
13; Mismatches 34
                                                                                       (Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                  4835 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IRR003593, AAA_ATPase.
InterPro; IRR003593, AAA_ATPase.
InterPro; IPR002035; VWF_A.
InterPro; IPR002035; VWF_A.
Fam; PR00004; AAA; 2.
SMART; SM03382; AAA; 5.
SMART; SM03237; VWF; 1.
ROSITE; PS50234; VWF; 1.
Chaperone; ATP-binding; Repeat; Nuclear;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nuclear
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POLY-ASN.
VWFA.
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ATP (POT)
ATP (POT)
ATP (POT)
ATP (POTE
ATP (POTE
ATP (POTE
ATP (POTE
                  PRT;
                                                                                                                                  Midasin (MIDAS-containing protein)
                                                               28-FEB-2003 (Rel. 41, Created)
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Best Local Similarity 32....
Best Local 39, Conservative
                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1134
1520
1846
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                                                                                                            (Rel. 41,
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4629 481
4835 AA;
                                                                                                                                                                                                                                                                      FROM N.A.
OBT5T1:
                                                                                                          28-FEB-2003
                                                                                                                                                                                                                                                                           SEQUENCE
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DOMAIN
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Streptococcus
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VATA_STRP3
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WAYIDQYLRNALDGNPISLDVKHKALVQLKCPPLLITS ->
GIYRPIFKKCTRWKSYISFRCKALSIVHIMPTFTYYI (IN
                                                                                                                                                                                                                                                                                                                                     MEDLINE-2124753; PubMed=1310198;
Marich J.E., Pontsler A.V., Rice S.M., McGraw K.A., Dubensky T.W.;
"The phylogenetic relationship and complete nucleotide sequence of
human papillomavirus type 35.";
Virology 186:770-776(1992).
-!- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF
VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2
PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH
CONTAINS BINDING SITES FOR BOTH PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP (POTENTIAL).

DPVS -> SSV (IN REF. 2).

QQ -> HE (IN REF. 2).

SESLETLIKPYCLYHHQCLSCSWG ->
NFKHITYYYIXNYXRYHGA (IN REF. 2).

CAKNRTIEKLLS -> VEKREQQLKTIDA (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001177; Papillom_B1.
Pfam; PF00519; E1.
Pfam; PF00524; E1.N: 1.
Early protein; DNA replication; Helicase; ATP-binding; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.6%; Score 84.5; DB 1; Length 637; llarity 29.6%; Pred. No. 4; Conservative 16; Mismatches 56; Indels 35
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=94265501; PubMed=8205838;
Dellus H., Hofmann B., in Primer-directed sequencing of human papillomavirus types.";
Curr. Top. Microbiol. Immunol. 186:13-31(1994).
                                                                                                                                                         Human papillomavirus type 35.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REF. 2).
V -> E (IN REF. 2).
D -> V (IN REF. 2).
; 3C694D4451791003 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                  01-AUG-1992 (Rel. 23, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
115-JUL-1998 (Rel. 36, Last annotation update)
Replication protein E1.
                                                         637 AA
                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               613 D
72122 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X74477; CAA52563.1; -. EMBL; M74117; AAA46968.1; -.
                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 470
34
143
258
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613 6
637 AA;
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                       NCBI_TaxID=10587;
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142
235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269
                                                                                                                                                                                         Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45;
                                                      VE1 HPV35
P27220;
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CONFLICT
SEQUENCE
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                          RESULT 8
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8 8

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This SWISS-PROT entry is copyright. It is produced through a collaboration
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---ETPT-- 124
                                        122 AKRRLFELPDSGYGNSEVEIQQIQQVEG-HDTVEQ-CSMGSGDSITSSSDERHDETPTRD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashi H., Hamada S.;
"The genome of invasive Streptococcus pyogenes; a comparative analysis of S. pyogenes SSI-1, SP370 and MGASS232.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Produces ATP from ADP in the presence of a proton gradient across the membrane. The V-type alpha chain is a
                                                                                                                                                                                                                        VATA STRP3 STANDARD; PRT; 591 AA.
Q8K8T1; Q879P3;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
V-type ATP synthase alpha chain (EC 3.6.3.14) (V-type ATPase subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22133808; PubMed=12122206;
Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
"Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 catalytic subunit.
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H(+) (Out).
SIMILARITY: Belongs to the ATPase alpha/beta chains family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=SSI-1 / Serotype M3;
Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; ATP synthesis; Hydrogen ion transport; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                  ATPA OR NTPA OR SPYN3 0120 OR SPS0122.
Streptococcus pyogeneB (serotype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
  79 AK--IFEPPAPGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002)
                                                                                                        180 IIQILKCSNANAAMLAKFKE---LFG-ISFTE 207
                                                                                125 ---IQKGSYTFVPWLLSFKRGSALYGQVLYTD 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD001099; ATPASE AC; 1.
PROSITE; PS00152; ATPASE ALPHA BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP; MF 00309; -; 1.
InterPro; IPR000793; ATPase_a/bC.
InterPro; IPR000194; ATPase_a/bcentre.
InterPro; IPR004100; ATPase_a/bN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE014138; AAM78727.1; ALT_INIT.
EMBL; AP005141; BAC63217.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PP00006; ATP-8ynt ab; 1.
Pfam; PP00306; ATP-8ynt ab C; 1.
Pfam; PP02874; ATP-8ynt ab N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Serotype M3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=198466;
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Query Match
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EMBL;
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ID KPCE
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DT 01-M
            SO DE RESERVA DE RESER
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RC STRAINECT COURDAIN.

RAPET KE. ST. Schueller C., Wambutt R., Murphy G., Volckaert G., Rabiller C., Wambutt R., Entian K.-D., Terryn N., Herris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Muclard B., Macher B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., RA Reichert B., McUllagh B., Bilham L., Robben J., Vandenbussche F., Raeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E., Raeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E., Weitzengger T., Bothe G., Ramsperger U., Hilbert H., Braun M., Raerieser S., Hempel S., Van Staveren M., Dirkse W., Moijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., RA De Keyser S., Hempel S., Feldpausch M., Lennerth S., Van Gerz G., Cronin A., Quail M., Bray-Allen S., Allen M., Rogers J., Cronin A., Quail M., Bray-Allen S., Rap Pettett A., Rajandream M.A., Lyne M., Lennard M., McLay K., Mayes R., RA Borkova D., Blocker H., Schaffe M., Grimm M., Lochnert T. H.,
RA Borkova D., Blocker H., Schaffe M., Grimm M., Mehler S.,
                                                                                                                                                                                                                                                                                                                                                            403
                                                                                                                                                                                                                                      328 MADSTSRWAEALREMSGRLQEM------PGDEGYPAYLGS---RIAEYYERAGRVRT 375
                                                                                                                                                                                                                                                                                                                                                                                                                   ODCLOLIA---DSETPTIQKGSYTFVPWLLSFKRGSALYGQVLYTDKTYAMGHLIQRKK- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKES-PSVLLSCCLTVVSFYQVAA---- 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 ----LQGDLASLRAELQGHHAEKLPAGAKIFEPPAPGEGNSSQNSRNKRAVQGPEETVT
                                                                                                                                                                                                                                                                                                                                                         376 LGSQEREGTITAIGA-----VSPPGGDISEP--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----VHVFGDELSLVTLFRCI--QNLEEGDELQLAIPR-----ENAQISLD
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shuai B., Reynaga-Pena C.G., Springer P.S., "The LATERAL ORGAN BOUNDARIES gene defines a novel, plant-specific gene family.";
                                                                                                                         90;
                                                               7.5%; Score 84; DB 1; Length 591; 22.0%; Pred. No. 4;
                                                                                                                         71; Indels
      591 AA; 64982 MW; 296ADCD372009340 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
LOB domain protein 30.
LBD30 OR AT4G00220 OR F6N15.4.
                                                                                                                         30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
STRAIN=cv. Columbia,
MEDLINE=22063719; PubMed=12068116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant Physiol. 129:747-761 (2002).
                                                                                                                         54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                 Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 GDVTF 211
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081323;
SQ SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                      111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167
                                                               Query Match
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LD LB30 ARATH
LD LB30 ARATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 LSFKRGSALYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNLEEGDELQLAI 196
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Gabel C., Fuchs M., Fartmann B., Granderath K., Danner D., Herzl A., Meumann B., Argirliou A., Vitale D., Liguori R., Piravandi E., Massenet O., Quigley F., Clabauld G., Mundlein A., Felber R., Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S., Chefdor F., Cooke R., Baerger C., Monfort A., Casacuberta E., Gibbons T., Weber N., Vandenbold M., Barques M., Terol J., Torres A., Perishman D., Haber B., Bent E., Johnson S., Tacon D., Jesse T., Heijren L., Schwarz S., Scholler P., Heber S., Francs P., Blelke C., Prishman D., Haber M., Wilson R.K., de la Bastide M., Habermann K., Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K., Parnell L., Dedhia N., Gnoj L., Schutz K., Hung E., Spiegel L., Schon M., Murray J., Sheet P., Cordes M., Abu-Threideh J., Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J., Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D., Minx P., Bentley D., Fulton B., Miller M., Greco T., Kemp K., Melson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D., Antoniu B., Zidanic M., Stonekher M., Matero A., Shah R., Antoniu B., Zidanic M., Stonekher M., Matero A., Shah R., Swaby I.K., O'Ghushmessy A., Rodriguez M., Hoffman J., Till S., Chen M., Martienssen R., Mccombie W.R., Codtin M., Johnson A., Chen B., Marra M., Martienssen R., McCombie W.R.;

Le Marra M., Martienssen R., McCombie W.R.;

Le Marra M., Martienssen R., McCombie W.R.;

Le Marra M., Martienssen R., McCombie W.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 402., Nature 402.)
Nature 402., SPECIFICITY: Expressed in roots, stems, leaves and flowers.
-!- TISSUE SPECIFICITY: Expressed in roots, stems, leaves and flowers.
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tive 23; Mismatches
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P09216;
01-MAR-1989 (Rel. 10, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF43232; AAL27613.1; -.
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InterPro; IPR004883; DUF260.
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PROSITE; PS50891; LOB; 1.
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TNFA LAMGL P59694;
                              ACT SITE
MOD RES
MOD RES
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                                                                                  SEQUENCE
                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNFA_LAMGL
                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
     SILLES
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                                                                                                                                                                                                                                                                            X MEDLINE-88083621; PubMed=3691811;
A Ono Y., Fujii T., Ogita K., Kikkwa U., Igarashi K., Nishizuka Y.;
A Dion Y., Fujii T., Ogita K., Kikkwa U., Igarashi K., Nishizuka Y.;
A I'dentification of three additional members of rat protein kinase C family: delta- epsilon- and zeta-subspecies.";
L FEBS Lett. 226.125-128 (1987).
- ''- FUNCTION: THIS IS CALCTUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
- 'SERINE- AND THREONINE-SPECIFIC ENZYME.
C ''- FUNCTION: PRC IS ACTIVATED BY DIACKIGIVEROL WHICH IN TURN
- PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
C '- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
- I SIMILARITY: Contains 1 C2 domain.
C '- SIMILARITY: WELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                             Eŭkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                              Ono Y., Fujii T., Ogita K., Kikkawa U., Igarashi K., Nishizuka Y., "The structure, expression, and properties of additional members of the protein kinas C family.", Islon. 263:6927-6932(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST. PROSITE; PS00108; PROTEIN FINASE ST. SEPPERT, ATP-binding; Pransferase; Phosphorylation; Serine/threonine-protein Kinase; Phorbol-ester binding; Zinc;
01-MAR-1989 (Rel. 10, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Protein Kinase C, epsilon type (EC 2.7.1.-) (nPKC-epsilon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C2 DOMAIN.
PHORBOL-ESTER AND DAG BINDING
PHORBOL-ESTER AND DAG BINDING
PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDB; 1GMI; 25-OCT-01.
InterPro; IRR000008; C2.
InterPro; IRR00219; DAG PE-bind.
InterPro; IRR000519; Pkinase_C.
InterPro; IRR000719; Prot kinase.
InterPro; IRR002290; Ser_thr_pkinase.
Pfam; PP00168; C2; 1.
Pfam; PP00130; DAG_PE-bind; 2.
Pfam; PP00433; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMÄRT; SM00133; S_TK_X; 1.
SMÄRT; SM00220; S_TKG; 1.
PROSITE; PSS0004; C2 DOMAIN 2; 1.
PROSITE; PS00479; DAG PE_BIND_DOM_1; 2.
PROSITE; PS50081; DAG PE_BIND_DOM_2; 2.
PROSITE; PS00107; PROTEIN KINĀSE_ĀTP; 1
                                                                                                                                                                                MEDLINE=88198270; PubMed=2834397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probom; PD000001; Prot_kinase; 1.
SMART; SM00109; C1; 2.
SMART; SM00239; C2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pram; PF00433; pkinase C; 1.
PRINTS; PR00008; DAGPEDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M18331; AAA41872.1; -.
                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99
220
292
668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; B28163; KIRTCE
                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PKC SUBFAMILY
                                                 PRKCE OR PKCE.
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2.2.4

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Onuma M.;

Conting and sequence analysis of cytokine CDNAs of llama and camel.";

"Clothing and sequence analysis of cytokine CDNAs of llama and camel.";

"Conting and sequence analysis of cytokine cDNAs of llama and camel.";

"TWRSF1B/TWFR. It is mainly secreted by macrophages and can induce cell death of certain tumor.cell lines. It is potent pyrogen causing fever by direct action or by stimulation of interleukin I secretion and is implicated in the induction of cachexia, Under certain conditions it can stimulate cell proliferation and induce cell differentiation (By similarity).

--- SUBBUIT: Homotorimer (By similarity).

--- SUBBUITS CATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---EETVTQDC 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 L--QLIADSETPTIQKG-----SYTFVPWLLSFKRGSALYGQVLYTDKTYAMGHLIQ 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382 TDGQLASPGENGEVRQGQAKRLGLDEFNFIKVLGKGSFGKVMLAELKGKDEVYAV--KVL 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 RKKVHVFGDELS------EGDELQLAIP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      440 KKDVILQDDDVDCTMTEKRILALARKHPYLTQLYCCFQTKDRLFFVMEYVNGGDLMFQIQ 499
                                                                                                                                                                                                                                                                                                                                                                                                                            19 REEMKLKECVSILPRKESPSVLLSCCLTVVSFYQVAALQGDLASLRAEL--QGHHAEKLP 76
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
14-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
11-SEP-2003 (Rel. 42, La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteolytic processing (By similarity).

PTM: The membrane form, but not the soluble form, is phosphorylated on serine residues. Dephosphorylation of the membrane form ocurrs by binding to soluble TNFRSFIA/TNFRI (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

PHOSPHORYLARION (AUTO-) (POTENTIAL)

PHOSPHORYLATION (AUTO-) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Raadan O., Lee S., Yoshida R., Chang K., Ohashi K., Sugimoto C.,
                                                                                                                                                                                                                                                                                                                                                 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostor
Mammalia, Eutheria, Cetartiodactyla, Tylopoda, Camelidae, Lama
                                                                                                                                                                                                                                                                       7.4%; Score 82.5; DB 1; Length 737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                 88; Indels
   422 ATP (BY SIMILARITY).
437 ATP (BY SIMILARITY).
532 BY SIMILARITY.
703 PHOSPHORYLATION (AUTO-) (F
710 PHOSPHORYLATION (AUTO-) (F
83478 MW; 6AD6999EFDD2659F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 AGAKIFEPPAPGEGNS-SQNSRNKRAVQGP----
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                                                                                                                                                                                                                                                                                                                                                 34; Mismatches
                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-SEP-2003 (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                          20.7%;
                                                                                                                                                                                                                                                                                                                                                 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                      532
703
710 7
737 AA;
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R 198
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                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 EGNSSQNSRNKRAVQGPEETVTQDCLQ-----LIA-----DSETPTIQKGSYTFVP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 LRSSSQASRDKPVAHTVVADPAAQGQLQWEKRPANTLLANGVKLEDNQLVVPTDGLY---- 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
                                                                                                                                                                                                                                                                                                                                                                                                                                          16
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|PKKAGGPQGSRRCLCLSLFSFLLVAGATTLFCLLHFGVIGPQKEELLTGLQIMNPLAQT
                                                                                                                                                                                                                                                              EXTRACELLUIAR (POTENTIAL).
PHOSPHORYLATION (BY CK1) (BY SIMILARITY)
CLEAVAGE (BY ADAM17) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                               31 LPRKE-SPSVLLSC-CLTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAKIFEPPAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 WLLSFKRGSALYGQVLYTDK----TYAMGHLIQRKKVHVFGDELSLVTLFR--C----
                                                                                                                                                  Cytokine, Transmembrane, Signal-anchor, Phosphorylation.
CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM (BY SIMILARITY).
                                                                                                                                                                                                           SIMILARITY).
CYTOPLASMIC (POTENTIAL).
SIGMAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(BY SIMILARITY).
                                                                                                                                                                                             (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93301617; PubMed=8315394;
Fritzler M.J., Hamel J.C., Ochs R.L., Chan B.K.L.;
"Molecular characterization of two humn autoantigens: unique cDNAs
encoding 95- and 160-kD proteins of a putative family in the Golgi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                             TUMOR NECROSIS FACTOR, SOLUBLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 EEAEAKPWYEPIYLGGVFQLEKDDRLSAEINMPNYLDFAESGQVYFGIIAL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Exp. Med. 178:49-62(1993).
-!- FUNCTION: GOLGI AUTO-ANTIGEN; MAY HAVE A FUNCTION IN THE PROCESSING AND TRANSPORT OF PROTEINS THROUGH THE GOLGI.
-!- DOMAIN: EXTENDED ROD-LIKE PROTEIN WITH COLLED-COIL DOMAINS.
-!- SIMILARITY: HIGH, TO RAT CIS-GOLGI MATRIX PROTEIN GM130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----IQNLEEGDELQLAIPRENAQISLDGDVTFFGALKL
                                                                                                                                                                                                                                                                                                                                                     7.3%; Score 82; DB 1; Length 233; 22.5%; Pred. No. 1.9; ive 29; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                             F5C07837505FBD86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            620
                                                                                                                                                                                                                                                                                                                BY
                                                                                                       EMBL; AB107646; BAC75383.1; -. PROSITE; PS00251; TNF 1; 1. PROSITE; PS50049; TNF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                             25437 MW;
                                                                                                                                                                                                                                                                                                                                                                                     52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35,
01-NOV-1997 (Rel. 35,
28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                             233 AA;
                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
                                                                                                                                                                                                                          DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                             DISULFID
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Q08379;
                                                                                                                                                                                                                                                                     DOMAIN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ASLRAELQGHH----AEKLPAGAKIFEPPAPGEGNSSQNSRNKRAVQGP--- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                           3 DSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVLLSCCLTVVSFYQ--VAALQGDL
                                                                                                                                                                                                                                                                                                                                                                                                             DGLDREE-----EEDEEBEEERAVAVPQPMPSIPEDLESREAMVAFFNSAVASAEEEQ
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mushinski J.F.;
"The catalytic domain of PKC-epsilon, in reciprocal PKC-delta and epsilon chimeras, is responsible for conferring tumorgenicity to NH13T3 cells, whereas both regulatory and catalytic domains of PKC-epsilon contribute to in vitro transformation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT, SERINE- AND THREONINE-SPECIFIC ENZYME. FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                           20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Last sequence update)
8-EFBS-2003 (Rel. 41, Last annotation update)
Protein kinase C, epsilon type (EC 2.7.1.-) (nPKC-epsilon).
PRKCE OR PKCEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=89137541; PubMed=2917656;
Schaap D., Parker P.J., Bristol A., Kriz R., Knopf J.;
"Unique substrate specificity and regulatory properties of PKC-epsilon: a rationale for diversity.";
FEBS Lett. 243:351-357(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang Q.J., Acs P., Goodnight J., Blumberg P.M., Mischak H.,
Mushinski J.F.;
as its content
                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----EETVTQDCLQLIADSETPTIQKGSY 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wheeler D.L.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                      54B31A0FBB42BFC8 CRC64;
                                                                                                                                                                                         COILED COIL (POTENTIAL)
COILED COIL (POTENTIAL)
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                           52;
                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                            Pred. No. 6.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     737 AA
                                                                                                                                                                                                                                                                                                                                           20; Mismatches
non-profit institutions as long
                                                                                                                                                                                                                                                                                                        7.3%; Score 82;
                                                  or send an email to license@igb-sib.ch)
                                                                                                                                            MIM; 602580; -.
GO; GO:0005794; C:Golgi apparatus; TAS.
                                                                                                                                                                                                                                                     POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98127436; PubMed=9467942;
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                                                                                                                                                                                                                                                                      70472 MW;
                                                                                    EMBL; 106147; AAA35920.1; -. PIR; JH0821; JH0821.
                                                                                                                                                                                                                                                                                                                          25.2%;
                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                         Genew; HGNC:4425; GOLGA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                               510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   musculus (Mouse)
                                                                                                                                                                              Golgi stack, Coiled
                                                                                                                                                                                                                                                                        620 AA;
                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                             41;
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                                                                                                                                                                                                                                                                          SEQUENCE
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Best Local
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                               440 KKDVILQDDDVDCTMTEKRILALARKHPYLTQLYCCFQTKDRLFFVMEYVNGGDLMFQIQ 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 PAPRRGAQLRRHKTKKNVRLTKKPHSGLPVPTKLQTFLTRRAEDBFTTMRYSAVTCDPTD 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 L--SFKRGSALYGQ------VLYTD-----KTY-----AMGHLIQRKKVHVFGDE-- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 ----LSLVT------LFRCI------QNLEEGDELQLAIPRENAQISLDGDV 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xoconostle-Cazares B., Leon-Ramirez C., Ruiz-Herrera J.;
"Two chitin synthase genes from Ustilago maydis.";
Microbiology 142:377-387(1996).
in the control of the cont
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                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Chitin synthase 1 (EC 2.4.1.16) (Chitin-UDP acetyl-glucosaminyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ustilago maydis (Smut fungus).
Bukaryota; Pungi, Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
NCBI_TaxID=5270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X87748; CAA61027.1; -.
PIR; S55520, S55520.
InterPro; IPR004834; Chitin_synth.
Pfam; PF01644; Chitin_synth; 1.
ProDom; PD002998; Chitin_synth; 1.
Transferase; Glycosyltransferase; Transmembrane; Cell wall; SEQUENCE 760 AA; 85181 MW; 9377000F57410993 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58; Indels

    -!- SUBCELLULAŘ LÓCATION: Plasma membrane-bound.
    -!- SIMILARITY: BELONGS TO THE CHITIN SYNTHASE FAMILY.

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Local Similarity 21.1%; Pred. No. 9.5;
nes 39; Conservative 33; Mismatches 58;
                                                                                                                                                                                                                                                                                                               760 AA
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STRAIN-RK32 / A2B3;
MEDLINE=97086517; PubMed=8932711;
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                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the the buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- EETVTQDC 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382 TDGOLASPGENGEVRPGQAKRLGLDEFNFIKVLGKGSFGKVMLAELKGKDEVYAV--KVL 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 RKKVHVFGDELS-----BGDELQLAIP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325 AGA---ESPQPASGNSPSEDDRSKSAPTSPCDQELKELENNIRKALSFDNRGEEHRASSA 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:97599; Prkce.
GO; GO:0004699; F:calcium independent protein kinase C activity; IDA
   PKC ALSO SERVES AS
                                                                                                                   SIMILARITY: Contains 1 C2 domain.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
PKC SUBFAMILY.
PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. FKC ALSO SERVES THE RECEPTOR FOR PROMOTERS, A CLASS OF TUMOR PROMOTERS. SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.3%; Score 81.5; DB 1; Length 737; 20.7%; Pred. No. 9.1; ive 33; Mismatches 89; Indels 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002019; C2.
InterPro; IPR002019; DAG PE-bind.
InterPro; IPR002019; DAG PE-bind.
InterPro; IPR000219; Prot kinase.
InterPro; IPR000219; Prot kinase.
InterPro; IPR000209; Ser_kr_pkinase.
Pfam; PF00168; C2; 1.
Pfam; PF00168; C2; 1.
Pfam; PF00433; pkinase, 1.
Pfam; PF00433; pkinase, 1.
ProDom; PF000001; Prot kinase; 1.
SWART; SM00109; C1; 2.
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Best Local Similarity
Matches 50; Conserv
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Search completed: February 3, 2004, 07:44:14 Job time : 12.2044 secs

us-09-911-777-1.rsp

86.5 7.8 3551 11 Q99PS4 86.5 7.8 3576 11 Q9QZW2 85 7.6 213 16 Q9JUY1 85 7.6 475 6 Q8WMX8	7.6 475 11 09UHF9 5 7.6 388 16 08R9D3 5 7.6 1653 5 Q9VSM1 5 7.6 179 5 Q9VSM0 5 7.6 2136 4 Q8NFU7 1 7.5 563 16 Q9SLI9	84 7.5 563 84 7.5 563 83.5 7.5 360 83.5 7.5 596 83.5 7.5 693 83 7.4 384	83 7.4 591 16 Q9A1Q3 83 7.4 694 3 QBTFL0 83 7.4 809 11 Q8CDE6 82 7.3 990 4 Q9NYF9 81.5 7.3 315 15 Q9WQ43	81.5 7.3 325 15 Q9WHV9 Q9whv9 mouse 81 7.3 177 10 Q9M511 Q9M511 Oryza 81 7.3 315 15 Q83411 Q83411 mouse 81 7.3 315 15 Q83400 Q83401 mouse 81 7.3 315 15 Q83400 Q83400 mouse	ALIGNMENTS SULT 1 ZIG DEBITMINABY. DPT. 208 AA	MAR-2003 (TrEMBLrel. 23, Created) MAR-2003 (TrEMBLrel. 23, Last sequence MAR-2003 (TrEMBLrel. 23, Last sequence MAR-2003 (TrEMBLrel. 23, Last annotat; MAR-2003 (TrEMBLrel. 23, Last annotat; Marbocyte stimulator (Fragment). SF13B. o sapiens (Human). aryota; Metazoa; Chordata; Craniata; aryota; Autheria; Primates; Catarrhini. I_TaxID=9606;	[1] [2] [3] [4] [5] [5] [6] [6] [7] [7] [7] [8] [8] [8] [9] [9] [9] [9] [9] [9] [9] [9] [9] [9	Similarity 75.0%; Pred. No. 6e-69; 6; Conservative 0; Mismatches 1; Indels SLRAELQGHHAEKLPAGAKIFEPPAPGEGNS SLRAELQGHHAEKLPAGA
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	otein - protein search, n: February 3,	Title: US-09-911-777-1 Perfect; score: 1116 Sequence: 1 MDDSTEREQSRLTSCLKKREENAQISLDGDVTFFGALKLL 218 Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 830525 segs, 258052604 residues Total number of hits satisfying chosen parameters: 830525 Minimum DB seg length: 0	ocessing: Minimu Maximu Listir	Database : SPTREMBL_23:* 1: sp_archea:* 2: sp_bacteria:* 3: sp_fungi:* 4: sp_human:* 5: sp_invertebrate:* 6: sp_innem:* 7: sp_mhman:*		Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES Result Query No. Score Match Length DB ID	750.5 67.2 208 4 QBIZIG 677 60.7 174 4 QBIZIG 610 54.7 258 11 QBBZMB 596 53.4 (158 4 QBIZI4 497.5 42.6 199 11 QBBWP2 249.5 22.4 194 11 QBBWP2 249.5 22.4 194 11 QBBWB2 152 13.6 25.9 4 QBIZM7 140.5 12.6 330 4 QBIZM7 91.5 8.2 267 16 Q9BBG7 91.5 8.2 267 16 Q9BBG7 91.5 8.2 267 16 Q9BMC7 87.5 7.8 1746 10 Q9AXNO 87.5 7.8 1524 10 QBRYNZ

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206 DGDVTFFGALKLL 218
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246 NGDDTFFGALKLL 258
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                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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nes 123;
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SEQUENCE
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MEDINES=22354631; PubMed=1246681;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I all Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AK034121; BAC28593.1; -.
                                                                                                                                                                                                                                                                                                                                                                                          80 KIFEPPAPGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSF
                                                                                                                                                                                                                                                                                                                                                                                                          2 KIFEPPAPGEGNSSQNSRNKRAVQGPESTVTQDCLQLIADSETPTIQKGSYTFVPWLLSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 LLSCCLTVVSFYQVAALQGDLASLRAELQGHH-----AEKLPAGAKIFEPPAPGEG
                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 IONMPETLENNSCYSAGIAKLEEGDELOLTIPRENAOISLOGDVTFFGALKLL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                           Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                             34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 54.7%; Score 610; DB 11; Length 258; Best Local Similarity 53.0%; Pred. No. 2.3e-54; Matches 134; Conservative 17; Mismatches 28; Indels 7
                                                                                                                                                                                                                                                                                                                                   Length 174;
                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                He F., Gao H., Li R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AY129227; AAN08423.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28604 MW; E6431FE93E782810 CRC64;
                                                                                                                                                                                                                                                                                                      174 AA; 19479 MW; 1AEBD4F2862EB3E0 CRC64;
                                                                              01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
B-lymphocyte stimulator (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ol-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Tumor necrosis factor (Fragment).
                                                                                                                                                                                                                                                                                                                                60.7%; Score 677; DB 4;
79.8%; Pred. No. 1.7e-61;
iive 0; Mismatches 1;
                                                                    174 AA
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181 ELQLTIPRENAQISLDGDVTFFGALKLL 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 79.8
Matches 138; Conservative
                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               140 KRGSAL-
                                                                                                                                                                                                                                                                                         NON TER
SEQUENCE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                     QBIZIS
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162
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--VTQDCLQLIAD 119
                                                                                                                                                                                      -----LEEGDELOLAIPRENAQISL 205
                                                                                                                                                                                                                 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                             ----YGQVLYTDKTYAMGHLI
                                                                                                                      1 NSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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SEQUENCE FROM N.A.
Schneider K., Kolthow S., Schneider P., Goebel T., Kaspers B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 NSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 -----YGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        He F., Gao H., Li R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX129228; AAN08424.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 AA; 17826 MW; 8346BCC0D333DCAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----LEEGDELQLAIPRENAQISLDGDVTFFGALKLL 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel. 22, Created)
U-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
TNF family B cell activation factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.4%; Score 596; DB 4;
llarity 77.8%; Pred. No. 3.2e-53;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               288 AA
                                                                                                                                                                                        163 QRKKVHVFGDELSLVTLFRCIQN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created 01-MAR-2003 (TrEMBLrel. 23, Last set 01-MAR-2003 (TrEMBLrel. 23, Last an B-lymphocyte stimulator (Fragment).
                                                                                               SETPTIOKGSYTFVPWLLSFKRGSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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PTIRKGS 186
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                  180
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                                                                                                               Q8BVA3
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                                                                                                                                                                                                                                                                                                                               61 TELEALRSELIYRVRARSPLEQPPVSPGDKKAGASVSSFLQVSAAGARQENRLPGPSPAF 120
                                                                                                                                                                                                                                                                                                                                                                       90 GNSSQ----NSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                    --YGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQN-- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 LEEQGNKIVIKETGYFFIYGQVLYTDTTFAMGHLIQRKKAHVFGDDLSLVTLFRCIQNMP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --VTQDCLQLIADSET 122
                                                                                                                                                                                                                                    -- FEPPAPGE 89
                                                                                                                                                                                                                  -----VLLSCCLTVVSFYQVAALQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,70 coll-length cDNAs."; Nature 420:563-573 (2002).

EMBL; AKOSO384; BAC34225.1; ... SEQUENCE 199 AA; 21654 MW; 39392021D4EFD320 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MDESAKTLPPPCLCFCSEKGEDMKV-GYDPITPQKEEGAWFGICRDGRLLAATLLLALLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 CCLTVVSFYQVAALQGDLASLRAELQGHH-----AEKLPAGAKIFEPPAPGEGNSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Stacheli P.;
"A chicken homolog of the B cell activating factor of the TNP family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 22.6%; Score 252.5; DB 11; Length 199; Best Local Similarity 36.9%; Pred: No. 9.4e-18; Matches 69; Conservative 18; Mismatches 41; Indels 59;
                                                                                                                                   DB 13; Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 QSYPNNSCYTAGIAKLEEGDELQLTIPRRRAKISLDGDGTFFGAVRLL 288
                                                      Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MDDSTER-EQSRLTSCLKKREEMKLKECVSILPRKESPS-----
                                                                          EMBL, AF506010; AAM90951.2; -.
SEQUENCE 288 AA; 31629 MW; 8E2F291D2495BB79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                     Pred. No. 9.8e-43;
                                                                                                                               //Match 44.6%; Score 497.5; I Local Similarity' 41.7%; Pred. No. 9.8e-ies 120; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                22 MKLKECVSILPRKE---SPS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Liver;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                          58 GDLASLRAELQGHHAEKLP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor necrosis factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 PTIQKGS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186
                                                                                                                                     Query, Match
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---- VTQDCLQLIADSET 122
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                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22254683; PubMed=1246681;
The FANTOM Consortium.
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK079180; BAG27571.1;
SEQUENCE 194 AA; 20961 MW; 85FCF3495B138377 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Makaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalla, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genomic structure of APRIL, a proliferation-inducing ligand.";
"Genomic structure of APRIL, a proliferation-inducing ligand.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AFSI350.11, AAM47279.1;
InterPro; IPR006052; TNF_family.
Pfam; PF00229; TNF; 1.
PROSITE; PS00251; TNF 1; 1.
PROSITE; PS00251; TNF 1; 1.
PROSITE; PS0049; TNF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.4%; Score 249.5; DB 11; Length 194; 36.4%; Pred. No. 1.9e-17; ive 19; Mismatches 41; Indels 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Koyama T., Tsukamoto H., Masumoto K., Himeji D., Hayashi K.,
Harada M., Horluchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MDDSTER-EQSRLTSCLKKREEMKLKECVSILPRKESPS-----
                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ol-UCT-2002 (TrEMBLrel. 22, Last sequence update) 01-WAR-2003 (TrEMBLrel. 23, Last annotation update) Proliferation-inducing ligand APRIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 CCLTVVSFYQVAALQGDLASLRAELQGHH-----
   194 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 AA
                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J; TISSUE=Urinary bladder;
                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                         (TrEMBLrel. 23, (TrEMBLrel. 23, (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                Tumor necrosis factor.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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(TrEMBLrel.
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                                                                                                                                                   Hahne M.;
                                                                                                                                                                                                                                                                                                                                                                                         185
                                                                                                                                                                                                                                      Query Match
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                                                                                                                           -----NSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFK 140
                                                                                                                                                  EOSSDALEAWENGERSKKRRAVLTOKOKKOHSVLHLVPINAT-SKDDSDVTEVMWOPALR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVAALQGDLASLRAE---LQGHHAEKLPAGAKIFE----PPAPGEGNSSQNSRNKRAV 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 DTGIYLLYSQVLFHDVTFTMGQVVSRE-----GGGRRETLFRCIRSMPSDPDRAYNSCY 372
                                                                           90
                                                                                                  84
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUB-Retina;
STRAIN-C57BL/6J; TISSUB-Retina;
MEDLINE-22334681; DubMed=12466851;
The FANTOM Consortium.
The RIKEN Genome Exploration Research Group Phase I & II Team;
Thanlyais of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
BRUL; AK044387; BAC31897.1; -.
SEQUENCE 410 AA; 45881 MW; 590A4B74C33FBBD4 CRC64;
                                                                                          -----LYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 ÓLRLCÓTELOSLRREVSRLÓRSGGPSOKOGERPWOSLWEOSÞDVLEAWKDGAKSRRRRAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 QGPEETVTQDCLQLI-----ADSETPTIQKGSYTFVPWLLSFKRGSA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 LTQKHKKKHSVLHLVPVNITSKADSDV-----TEVMWQPVLRRGRGLEAQGDIVRVW
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                          -----NLEEGDELQLAIPRENAQISLDGDVTFFGALKL 217
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                                         41 LSCCLTVVSFYQVAALQGDLASLRAE---LQGHHAEKLPAGAKIFEPPAPGEG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 410;
                           Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 ----LYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71; Indels
  AE1E4FDEFD578898 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----NLEEGDELQLAIPRENAQISLDGDVTFFGALKL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            373 SAGVFHLHQGDIITVKIPRANAKLSLSPHGTFLGFVKL 410
                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 11;
                         13.6%; Score 152; DB 4; 24.9%; Pred. No. 2.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.1%; Score 146; DB 11
26.1%; Pred. No. 2.3e-06
                                                                                                                                                                                                                                                                                                                  Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24; Mismatches
                                                 31; Mismatches
                                                                                                                                                                                                                                                                                                                  410
                                                                                                                                                                                                                                                                                                                                          Created)
 27453 MW;
                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 23, (TrEMBLrel. 23, 1 (TrEMBLrel. 23, 1
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57; Conservative
                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                            RGSA----
                                                                                                                                                                                                                                                                                                                                                                               factor
                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
   250 AA;
                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                            ----0
                                                                                                                                                                                                                                                                                                                                                                               Tumor necrosis
                                                                                                                                                                                                                                                                                                                                          01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003
01-MAR-2003
                                                   28;
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   SEQUENCE
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                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                  Matches
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330 AA.

Q81ZK7, PRELIMINARY; PRT; Q81ZK7; 01-MAR-2003 (TrEMBLrel. 23, Created)

Q812K7

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11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "An endogenous hybrid mRNA encodes TWE-PRIL, a functional cell surface TWEAK-APRIL fusion protein."; EMBO J. 21:5711-5720(5002). EMBD: AVEO1651; AAL50443.1; -SEQUENCE 330 AA; 36588 MW; PC6F3BCA29C029AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE=21082930; PubMed=11214968; MEDINE=21082930; PubMed=11214968; MEDINE=21082930; PubMed=11214968; Meneko T., Nakammira Y., Sato S., Asamiru E., Kato T., Kanura T., Watanha A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Echara M., Matsumoto M., Matsumo A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuoli C., Yamada M., Tabata S.; "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti."; DNA Res. 7:331-338(2000).
EMBL; AP003007; BAB52105.1; -. InterPro; IPR001034; HTM DeoR.
PEMBL; PP00455; deoR: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 SSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 -----LYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tch 12.6%; Score 140.5; DB 4; Length 330; al Similarity 26.5%; Pred. No. 6.3e-06; 43; Conservative 24; Mismatches 52; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 267;
                                                                                                                                                                                                                                                                                                                                                   MEDLINE-22299924, PubMed-12411489,
Pradet-Balade B., Medema J.P., Lopez-Fraga M., Lozano J.C.,
Kolfschoten G.M., Picard A., Martinez-A C., Garcia-Sanz J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 NSCYSAGVFHLHQGDILSVIIPRARAKLNLSPHGTFLGFVKL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 AA; 29577 MW; 03E99717CA35F544 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----NLEEGDELQLAIPRENAQISLDGDVTFFGALKL
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

8.2%; Score 91.5; DB 16;
Best Local Similarity 21.2%; Pred. No. 0.51;
Matches 48; Conservative 39; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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    23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                         01-MAR-2003 (TrEMBLrel.
                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=MAFF303099;
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                                                                                                                                                                                                                               NCBI_TaxID=9606;
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PRELIMINARY;
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01-MAR-2003
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01-NOV-1996
                                 01-JUN-2001
                                                                                                                                                                                                                                                                            sets."
                                                                                                                                                                                                                                                                                                                                                              nterPro;
                                                                                                                                                                                                                                                                                                                                                                                  nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    nterPro;
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                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                  nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nterPro
                                                                                                                                                                                                                                                                                           J. Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS;
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                                                                 65 AELQGHHAEKLPAGAKIFEPP-----APGEGNSSQNSRNKRAVQGPEETVTQDCLQLI 117
                                                                                                                                   118 ADSETPTIQKGSYTFVPWLLSFKRGSALYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLV 177
                                                                                                                                                          95 GDGEPIIINGGTTTF--OMVHFLTGRRM---PIFTNSFPIAEHLLKHSKNTVM---LSGG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 RNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSPKRGSALY--GQVLYTDK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   535 STSRTIRHGD---VKPANILLTDKFIPKI---SYFGTSKLLTVDKDFTMFVVGSMGYIDP 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96
 64
                   | :: |:|:|
------ATIRRDIAALH 44
                                                                                                 45 VQ----KRLRRVRGGAEAISPPQFIGLAGRPFSVNETINASQKRA-----IAREAVELC 94
6 BREQSR-LTSCLKKREEMKLKECVSILPRKESPSVLLSCCLTVVSFYQVAALQGDLASLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 LLSCCLTV---VSFYQVAALQGDLASLRAELQGHHAEKLPAGAKIFEPPAPGEGNSSQNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       479 LIGCCLEVDVPMLVYEFAA-KGNLODI---LHGDANIPLPLGLRLNIAIESAEGLRYMHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 TY-AMGHLIQRKKVHVFGDELSLVTLFRCIQNLEEGDELQLAIPRENA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wing R.A.; Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo
Saski C., Henry D., Oates R., Simmons J.;
"Rice Genomic Sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (Rice).
Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracl
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                       TLFRCIQNLEEGDELQLAIPRENAQIS-LDGDVT-----FFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ubmitted (FEB-2002) to the EMBL/GenBank/DDBJ databases WBL; AC098565; AAL69427.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS01187; BGF CA; 1.
PROSITE; PS010107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; EGF-like domin; Kinase; Transferase.
SEQUENCE 695 AA; 77048 MW; D9DEFERAA74A655A5 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
8.2%; Score 91.5; D
Best Local Similarity 27.4%; Pred. No. 1.9;
Matches 46; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                              695
                     | | : | : | : | : | | : | | : | | 3 EKERHRIILSAVQEKPVVTVQEMVDLTESSE.
                                                                                                                                                                                                                                                                                                                                                                                                             Putative wall-associated protein kinase OSJNBA0028C16.9
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nterPro; IPR00290; Ser thr pkinase.
fam; PF00069; pkinase; I.
robom; PD000001; Prot kinase; 1.
vART; SM0019; BGP_CA; 1.
                                                                                                                                                                                                                                                                                                                                                                Created
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nterpro; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                           1-MAR-2002 (TrEMBLrel. 20,
1-MAR-2002 (TrEMBLrel. 20,
1-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4530;
                                                                                                                                                                                                                                       147 TIYR---
                                                                                                                                                                                                                                                                                            RESULT 12
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RESULT 13

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WLLSPKRGSALYGQVLYTDKTYAMGHLIQRKKVH--VFGD------ELSLVTLFRCI 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 PAGAKIFEPPAPGEGNSSQNSRNKRAVQGPEETVTQDCLQLIAD-SETPTIQKGSYTFVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 KLKECVSILPRKESPSVLLSCCLTVVSFYQVAALQGDLA-----SLRAELQGHHAEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----NPQDTVIEADQELVRSYYELPDDENSSANLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                  Stiller J.W., Riley J., Hall B.D.; "Are red algae plants? A critical evaluation of three key molecular
                                                                                                                                                                                      Eukaryota; Glaucocystophyceae; Gloeochaetales; Glaucosphaeraceae;
Glaucosphaera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 1746;
15;
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PROSITE; PS00115; RNA POL II REPEAT; 12.
SEQUENCE 1746 AA; 193767 WW; C0769A3392D6746D CRC64;
                                                                                                                 DNA-dependent RNA polymerase II largest subunit RPB1
                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57;
PRT; 1746 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.9%; Score 88; DB 21.8%; Pred. No. 15; tive 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PR000684; RNA_polII_repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002965; P rich extensn.
InterPro; IPR006592; RNA_polA_N.
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Hypothetical protein slr0120.
SLR0120.
                                                                    (TrEMBLrel. 17, (TrEMBLrel. 23,
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1260 AQKEPEKMAEGEE 1272
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Best Local Similarity 21.84
Matches 42, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                  Glaucosphaera vacuolata
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rch completed: February 3, 2004, 07:46:50 time : 33.0667 secs
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ALPWILAPNIKSALVFGREDSGLTNEELNQAHRFVRIPVHPQYPSL 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                            MEDLINE=96127529; PubMed=8590279; Kaneko T., Miyajima N., Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N., Sugiura M., Tabata S.; Sugiura M., Tabata S.; Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O. MAR. 2002 (TrEMBLrel. 20, Created)
01-MAR. 2002 (TrEMBLrel. 20, Last sequence update)
01-MAR. 2003 (TrEMBLrel. 23, Last sequence update)
Hypothetical 82.1 kDa protein.
P0681B11.1 OR B1085F01.16.
Oryza sativa (Rice), and
Oryza sativa (apponica cultivar-group).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae;
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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TIGREPARS; TIGR0050; TRNA_methyll; 1; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 240 AA; 26916 MW; FCIDEEA995F5C89A CRC64;
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, D64004, BAA10658.1; -.
EMBL, D64004, BAA10658.1; -.
InterPro; IPR004384; rRNA_methyl_1.
InterPro; IPR010137; SpoU methylase.
Pfam; PF00588; SpoU methylase; 1.
ProDom; PD001243; SpoU methylase; 1.
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                                           NCBI TaxID=1148
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61 ASLRAELQGHHA-----EKLPAGAKIFEPPAPGEGNSSQNSRNKRAVQGPEET 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 VIQDCLQ----LIADSETPTIQ-KGSYTFVPWLLSFKRGSALYGQVLYTDKTYAMGHLIQ 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 LKKREEMKLKE--CVSILPRKESPSVL------LSCCLTVVSFYQVAALQGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 748;
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                                                                                                                                                                                                     EMBL, AP003022, BAB78635.1; ---
EMBL, AP003302, BAB89980.1; --
Gramene, Q8M0N1; ---
InterPro, IPR001245, Tyr Dkinase.
InterPro, IPR001245; Tyr Dkinase.
InterPro, IPR001245; Tyr Dkinase.
Fram, PP00069, pkinase; 1.
PROSITE, PS50011; PROTEIN KINASE DOM; 1.
PROSITE, PS00109; PROTEIN KINASE DOM; 1.
PROSITE, Tyrotein, ATP-binding; Transferase.
SEQUENCE 748 AA; 82079 MW; E18542CC048E36F7 CRC64;
                                                                                 STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
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20.7%; Pred. No. 5.4;
iive 39; Mismatches
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TALL-1 prote tumour necro BAFF protein PRO738 polyp TACI-ligand

TNF and Apol ZTN4 protein Neutrokine-a neutrokine-a tumour necro B lymphocyte BLyS binding B Lymphocyte Neutrokine-a prote

polypeptide PRO738 prote

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ZTNF4 amino

tumour necro

Perfect score:

Segmence:

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Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

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Membrane bound BLy
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Human NTN-2 DNA se
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Young PR;
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TNFL1. Homo
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                                                                                                          3, 2004, 07:43:37; Search time 36.3333 Seconds (without alignments) 952.359 Million cell updates/sec
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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1 MDDSTEREQSRLTSCLKKRE.......BNAQISLDGDVTFFGALKLL 218
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                 GenCore version 5.1:6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                 - protein search, using sw model
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AAW93586
AAB28553
AAB08659
AAB08191
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AAW58391
AAY22221
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Gapop 10.0 , Gapext 0.5
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Match
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25-JUN-1998.
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                                                                                                                                                                                        polypeptide sequence. Tis polypeptides and antibodies are useful for identifying compounds which agonise and antibodies are useful for identifying compounds which agonise and antagonise Tis, and these can be enhance Tis activity (antagonist) and these can be enhance Tis activity (antagonist) can also be used to enhance Tis activity. Diseases or susceptibility to a disease can be diagnosed by determining the presence or absence of a mutation in the Tis protein. Tis polymucleotides are useful for locating genes associated with disease by hybridisation to chromosomes. Tis polypeptides and polymucleotides can be used, especially to raise an immune response (i.e. as vaccines) for the treatment of chronic and acute inflammation, arthritis, septicemia, autoimmune diseases (e.g. inflammatory bowel disease, psoriasis), transplant rejection.

C graft vs. host disease, infection, stroke, ischaemia, acute respiratory disease syndrome, restenosis, brain injury, AIDS, bone diseases, cancer (e.g. lymphoproliferative disorders), atherosclerosis, and Alzheimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 KENKILVKETGYPFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                           New tumour necrosis factor homologue, TL5 - useful for diagnosis and treatment of Alzheimer's disease, AIDS and cancer
                                                                                                                                                                             present sequence encodes a tumour necrosis factor homologue TL5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              systemic lupus erythematosis; Hashimoto's autoimmune thyroiditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; 63954; primate; rodent; mouse; T cell surface antigen; madagnosis; antigen-specific proliferation; cytokine production; immune response; autoimmune disorder; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 19; Length 285;
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93.4%; Score 1042.5; DB 1.
Best Local Similarity 76.5%; Pred. No. 1.1e-103;
Matches 218; Conservative 0; Mismatches 0;
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                                                                                                                                   Claim 10; Page 18; 23pp; English.
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                WPI; 1998-508494/44.
N-PSDB; AAV58894.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 AA;
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The present sequence is a human T cell surface antigen, designated 53954. The novel protein designated 63954 is expressed on T cells.

Protein 63954 can modulate antigen-specific proliferation and cytokine production on effector cells and may potentiate immune cell expansion or apoptosis. 63954 agonists or antagonists may also act as a co-stimulatory molecule for regulation of T cell mediated cell activation, and may cause a shift of T helper cell types, e.g. between Thi-and Th2. Antagonists of 63954 can be used to modulate immune responses in abnormal situations, e.g. autoimmune disorders, including rheumatoid arthritis, systemic lupus erythematosis (SLB), Hashimoto's autoimmune thyroiditis, as well as acute and chronic inflammatory responses in which T cell activation, expansion, and/or immunological T cell memory play an important role, such as chronic inflammation or tissue rejection. The products can also be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions, or degenerative conditions. The products can also be used for detection, diagnosis and drug screening.
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                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polypeptide, 63954 - used to develop products for treating e.g. autoimmune disorders, inflammation, tissue rejection, cancer or degenerative conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 285;
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Pred. No. 1.1e-103;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSV-
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97WO-US23321
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16-DEC-1997;
                                                                        17-DEC-1996;
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Matches 218;
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9

Gaps

, 19

Indels

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/note= "intracellular domain"
47.72
/note= "transmembroca"
                                  Location/Qualifiers
                                                                                                                              Claim 17; Fig 1; 104pp; English.
                                                                                        (HUMA-) HUMAN GENOME SCI INC.
                                                                                 96WO-US17957
                                                                           96WO-US17957
                                                   73..285
/note= "
                                                                                               Ni J, Yu G;
                                                                                                      WPI; 1998-272216/24.
                                                                                                          N-PSDB; AAV30934.
                           Homo sapiens
                                                             WO9818921-A1
                                                                           25-OCT-1996;
                                                                                 25-OCT-1996;
                                                                    07-MAY-1998,
                                                                                               Ebner R,
                                     Domain
                                            Domain
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61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEBAPAVTAGLKIFEPPAP 120 181 KENKILVKETGYPFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240 1 MDDSTEREGSRITSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60 88 GEGNSSONSRNKRAVOGPEETVTODCLOLIADSETPTIOKGSYTFVPWLLSFKRGSAL--LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGA------KIFEPPAP -----YGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCION----DB 19; Length 285; ------LEEGDELQLAIPRENAQISLDGDVTFFGALKLL 218 241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285 1e-103; 0; 1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSV 93.4%; Score 1042.5; 76.5%; Pred. No. 1.1e ive 0; Mismatches Tribouley C; AAY22221 standard; Protein; 285 AA delayed type sensitivity; therapy. Claim 1; Page 61; 69pp; English. Human TNFL1 protein sequence. Pot D, 98US-0212270. 97US-0068959. 98WO-US27474 16-SEP-1999 (first entry) Best Local Similarity 76.5 Matches 218; Conservative Kassam A, Lamson G, WPI; 1999-405508/34. (CHIR) CHIRON CORP. 285 AA; N-PSDB; AAX84620 drug screening. 22-DEC-1998; WO9933980-A2 16-DEC-1998: Homo Bapiens 30-DEC-1997; 08-JUL-1999. 45 AAY22221; Sequence Query Match 146 ò 셤 셤 셤 ઠ g 셤 ò ò ò The sequence is that of the neutrokine alpha protein.

Neutrokine alpha (NA) polypeptides modulate cell proliferation,

C differentiation, magration, cytotoxicity and cell death.

C differentiation, magration, cytotoxicity and cell death.

They can be used to treat e.g. tumour and itumour metastasis, infections

by bacteria, viruses and other parasites, immunodeficiencies,

c inflammatory diseases, lymphadenopathy, autoimmune diseases, graft

versus host diseases and to stimulate peripheral tolerance, destroy some

transformed cell lines, mediate cell activation and proliferation, and

are functionally linked as primary mediators of immune regulation and

c transformed cell lines, mediate cell activation and proliferation, and correction, myeloprotection, stem cell activation and immune enhancement

or suppression, myeloprotection, stem cell activation and theating and pulmonary fibrosis. They

correction inflammatory control and treatment of leukaemia. They can also

c including liver cirrhosis, osteoarthritis and pulmonary fibrosis. They

can also be used to regulate haematopoietic progenitor cells, e.g. to

can also be used to regulate haematopoietic progenitor cells, e.g. to

can differentiation of various haematopoietic progenitor cells, e.g. to

creasormation, activation of the HIV virus, garaft-hoots rejection, cerebral

creasorption, rheumatoid arthritis and cachexia (wasting or malnutrition).

They can also be used to treat e.g. autoimmune diseases such as multiple

creasorption, rheumatoid arthritis and cachexia (wasting or malnutrition).

They can also be used to treat e.g. autoimmune diseases such as multiple

creasorption, rheumatoid arthritis and sacrolossis, idiopathic pulmonary

fibrosis, idiopathic hyper-eosinophilic syndrome, endotoxic shock,

creasorption and release of histamine-mediated allergic reactions and immunication and endormany and each and each and each offerantial and harding and each offerantial and each offerantial and each offerantial and each offerance influence and infine and such as allergic asthma, rhinitis and eczema, inflammatory pulmonary diseases, rheumatoid arthritis, inflammation, degenerative and inflammatory arthropathies, aplastic ansemia, wyslodysplastic syndrome, subepithelial basement membrane fibrosis or adult respiratory distress syndrome. The products can also be used for detection, diagnosis and neutrokine alpha; cell proliferation; differentiation; migration; cytocoxicity;cell death; treatment; tumour; infection; inflammation; wound healing; immunodeficiency; autoimmune disease; graft rejection; fibrotic disorder; haematopoiesis; sepsis; shock; malaria; HIV; AIDS; acquired immune deficiency syndrome; rheumatoid arthritis; silicosis; cachexia; detection; diagnosis; drug screening. "extracellular domain"

TNFL1; human; TNFR superfamily; tumour necrosis factor ligand; TNF; tumour necrosis factor receptor; TNFR superfamily; cell proliferation; cell differentiation; cytokine production; immunoglobulin; hyperplasia; apoptosis inducer; activated T cell; autoimmune disease; inhibitor; myasthenia gravis; insulin-dependent diabetes mellitus; endotoxic shock; theumatorid arthritis; multiple sclerosis; systemic lupus erythematosus; tumour; proliferative disorder; neoplasia; dysplasia; immunocompetence; lymphoid organogenesis; bacterial resistance; contact hypersensitivity; New tumour necrosis factor ligands, useful for induction of cell death and/or proliferation of cells This sequence is the tumour necrosis factor (TNF) ligand family

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regulatory roles in cell proliferation and/or differentiation, e.g. they can induce production of cytokines, immunoglobulins, etc. A variety of diseases can be treated by modulating the activity of TNFL proteins, c.g. they can induce apoptosis of activated T cells but rescue resting c.g. they can induce apoptosis of activated T cells but rescue resting T cell from apoptosis. TNFL polypeptides can therefore be used to treat autoimmune diseases, such as myssthania gravis, insulin-dependent diabetes mellitus, rheumatoid arthritis, multiple sclerosis, and systemic clupus erythematosus. TNFL proteins also have tumour stimulating properties, so tumours can be treated by inhibiting the expression or activity of TNFL other proliferative disorders, such as neoplasias, dysplasias, and hyperplasia can also be treated using TNFL inhibitors. The TNFL polypeptides and polynucleotides can also be used to enhance or decrease TNF activity, thus providing therapeutic benefits such as induction of cell death, lymphoid organogenesis, or host bacterial cresistance, and inhibition of endocoxic shock, contact hypersensitivity, and its receptors play a major role in host defence and immunosurveillance. As such, there is a need to identify new members of TNFR families. This invention provides this need.
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         protein of the invention, designated TNFL1. The TNFL proteins play
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20; Length 285;
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93.4%; Score 1042.5; DB 2.
Best Local Similarity 76.5%; Pred. No. 1.1e-103;
Matches 218; Conservative 0; Mismatches 0;
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61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEBAPAVTAGLKIFEPPAP 120
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                                                                                                                                                   The present sequence represents human Kay-ligand, which is a member of the tumour necrosis factor (TNF) family of cytokines. Pharmaceutical compositions containing the Kay-ligand can be used to suppress or stimulate the immune system, especially to prevent or reduce the severity of autoimmune diseases or response to a tissue graft or to treat cancer. An agent capable of interfering with the Kay-ligand can be used to induce cell death. The Kay-ligand can also be used to identify
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                                                                         New human or murine Kay-ligands, members of the tumour necrosis
                                                                                                                                                                                                                                                                                                                        Length 285;
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                                                                                                                                                                                                                                                                                                                      Score 1042.5; DB 20
Pred. No. 1.1e-103;
0; Mismatches 0;
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                                                                                                                      Claim 12; Page 32; 41pp; English
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76.58;
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                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 76.5
Matches 218; Conservative
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                              WPI; 1999-243715/20.
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Tschopp J;
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This invention describes isolated Tumor Necrosis Factor (TNF) family receptor polypeptides: APO4, APO6 and APO9 or their active fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or thair active fragments. APO4 is useful for diagnosing prostate cancer thair active fragments. APO4 is useful for diagnosing prostate cancer by determining levels of APO4 in an individual Prostate cancer can also be treated using APO4 selective binding agents linked to a therapeutic moiety. APO4 polypeptides are also useful for identifying selective binding agents to the polypeptide/active fragment which is extracellular, or expressed on the cell surface. The binding is preferably performed in vivo. APO4 polypeptides/active fragments are also useful for screening for apoints and anteagonists by binding and observing the changer in APO4 activity. Effective pharmacological agents useful in diagnosis or treatment of disease are also identified using APO4 polypeptides/active fragments and APO4 signal transducer molecules that specifically interact with a cytoplasmic domain of APO4 and detecting a change in level of APO4 activity. The method is performed in vivo or in vitro. APO polypeptides are also luseful activity activity. The method is performed in vivo or in vitro. APO polypeptides are also luseful for diagnosis/treatment of developmental or gestational
                                                                                                                                                    New Tumor Necrosis Factor family receptor polypeptides and ligands useful for diagnosis and treatment of prostate cancer and developmental or gestational abnormalities
                                                                                                                                                                                                                                                               Claim 34; Fig 11A; 156pp; English.
                                                                          WPI; 1999-205191/17.
                                                                                                        N-PSDB; AAX23420
                     Chaudhary
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285 AA; Sequence

LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180 181 KENKILVKETGYPPIYGQVLYTDKTYAMGHLIQRKKVHVPGDELSLVTLFRCIQNMPETL 240 9 87 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLATLLLALLSCC --KIFEPPAP GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL--Gaps DB 20; Length 285; 241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285 ------LEEGDELQLAIPRENAQISLDGDVTFFGALKLL 218 Indels LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGA-----1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSV 1.1e-103; 93.4%; Score 1042.5; 76.5%; Pred. No. 1.1e 0; Mismatches Local Similarity 76.5 les 218; Conservative 45 61 88 121 146 186 Query Match Best Loca Matches g ઠે 셤 셤 ò 엄 ઠે 요 ઠે 8

AAB28553 standard; protein; 285 AA (first entry) 08-FEB-2001 Human TNFL1 **EEXEXEX**

Human; tumour necrosis factor like-1; TNFL1; tumour necrosis factor; TNF; immunosuppressive; antiarthritic; neuroprotective; dermatalogical;

human protein designated tumour necrosis factor like-1 (TNFL1). It may be used to induce cell death in tumours, to induce apoptosis of activated T cells, to induce inflammation, and to rescue resting T cells from apoptosis. TNF receptors are used to regulate the function of a TNF ligand which plays a role in apoptosis, inflammation, differentiation, or proliferation. Expression of the receptors can also be useful as markers for cancer, especially for colon cancer. Diseases which can be treated rheumatoid arthritis, cancer, septic shock, Crohn's disease and osteoporosis. The polynucleotides can be used in gene delivery vehicles, for the purpose of delivering a mRNA or oligonucleotide, full-length protein, fusion protein, polypeptide, or ribozyme, or single-chain antibody, into a cell. The newly identified receptor proteins play regulatory roles in cell proliferation and/or differentiation. The present sequence is given in a specification relating to an isolated gene therapy; effects of TNF-L or TNFR-L subgenomic polynucleotides within the cell receptors can also play a role in the negative regulation of osteoclastogenesis. Soluble TWR-1.1ke receptors can be useful in the neutralisation of TNF or TNF-1.1ke ligands. A TNF-1 protein can also bused to treat autoimmune diseases (myasthenia gravis and Gaps disorders. A TNF-L or TNFR-L subgenomic polynucleotide can also be delivered to subjects for the purpose of screening test compounds fthose which are useful for enhancing transfer of TNF-L subgenomic polynucleotides to the cell or for enhancing subsequent biological colon cancer; rheumatoid arthritis; septic shock; Crohn's disease; osteoporosis; autoimmune disease; myasthenia gravis; insulin-dependent diabetes mellitus. Tumor necrosis factor (TNF) and TNF receptor superfamily protein members TNF-L and TNFR-L, useful for enhancing or decreasing TNF activities such as inducing cell death and lymphoid organogenesis and proliferative 67; Score 1042.5; DB 21; Length 285; cytostatic; osteopathic; Indels ; Pred. No. 1.1e-103;); Mismatches 0; insulin-dependent diabetes mellitus), tumours, antiinflammatory; antidiabetic; Claim 1; Page 65; 77pp; English. ; 93.4%; 05-APR-2000; 2000WO-US09058. 99US-0286529 Best Local Similarity 76.5 Matches 218; Conservative 2000-665004/64. (CHIR) CHIRON CORP. 285 AA; WPI; 2000-665004/ N-PSDB; AAC63756. WO200060079-A2 05-APR-1999; Homo sapiens Tribouley C; Sequence Query Match

120 180 145 -----YGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQN----- 185 9 87 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC ---KIFEPPAP 88 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL--MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSV-LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGA---Н 45 121 146

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immunodeficiency; inflammatory disease; lymphadenopathy; dermatitis; autoimmune disease; graft versus host disease; immune regulation; severe combined immunodeficiency. **Linked agammaglobulinemia; kappa chain deficiency; B cell lymphoproliferative disorder; purpura; Wiskott-Aldrich syndrome; systemic lupus erhythematosus; myocarditis; idiopathic thrombocytopenia purpura; hemolytic anemia; neuritis; allergic encephalomyelitis; relapsing polychondritis; glomerulonephritis; rhumatic heart disease; multiple sclerosis; uveitis opthalmia; polyendocrinopathy; Reiter's disease; autoimmune pulmonary inflammation; myeloprotection; stem cell mobilization; leukemia.
181 KENKILVKETGYFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLYTLFRCIQNMPETL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "potential N-linked glycosylation site"
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                                                                                                                                                                                                Amino acid seguence of a human neutrokine-alpha polypeptide.
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                                     218
                                                  241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKIL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                "transmembrane domain"
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diagnose tumor and tumor metables, inflammatory diseases, diagnose tumor and tumor diagnoses, inflammatory diseases, lymphadenopathy, autoimmune diseases, graft versus host disease, to mediate immune regulation and inflammatory responses. Diseases which may be treated include severe combined immunodeficiency (SCID) -X-linked agammaglobulinemia, kappa chain deficiency, B cell lymphoproliferative disorder (BLDD), wiskott-Addrich syndrome, systemic lupus erhythematosus, idiopathic thrombocytopenia purpura, hemolytic anemia, dermatitis, allergic encephalomyelitis, myocarditis, relapsing polychondritis, cheumatic heart disease, glomerulonephiritis, multiple sclerosis, Neuritis, Uveitis Opthalmia, Polychondcrinopathies, Purpura (e.g. Henloch-Scoenlein purpura), Reiter's Disease, and Autoimmune enhancement or suppression, myeloprotection, stem cell mobilization, acute and chronic inflammatory control and treatment of leukemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, cytokine; THANK; tumour necrosis factor homologue; apoptosis; nuclear factor-KB; c-jun N-terminal kinase; shock; acute phase response; viral infection; radiation susceptibility; atherosclerosis; cancer; acute inflammatory condition, arthritis; allergy;
                                Novel cytokine neutrokine-alpha, its splicing variant, neutrokine-alpha SV polypeptides useful for treating tumor, tumor metastasis, microbial infections, immunodeficiency, inflammatory diseases, lymphoadenopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----YGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQN----
                                                                                                                                                                The present sequence represents a human neutrokine-alpha polypeptide. Neutrokine-alpha polypeptides are used to treat, prevent, prognose and diagnose tumor and tumor metastasis, infections by bacteria, viruses and other parasites, immunodeficiancias informations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21; Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------LEEGDELQLAIPRENAQISLDGDVTFFGALKLL 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of human cytokine designated THANK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.4%; Score 1042.5; DB 2.76.5%; Pred. No. 1.1e-103; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   versus host reaction; tumour cell.
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                                                                                                                                              Claim 18; Fig 1A-B; 414pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB08191 standard; Protein; 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 76.5
Matches 218; Conservative
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N-PSDB; AAA64427.
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1..46 /note= "intracellular domain"

Location/Qualifiers

/note= "extracellular domain"

/note= "transmembrane

73..285

(first entry)

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AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
                                                                                 type II transmembrane protein, B cell stimulatory factor, inflammatory disorder, immune disorder, rheumatoid arthritis, lupus and graft versus host disease.
                                                 Amino acid sequence of a human AGP-3 polypeptide
                                                                                                                                                                                                                                                                                                         11-FEB-2000; 2000WO-US03653
                                                                                                                                                                                                                                                          WO200047740-A2
                                                                                                                                                                                                                                                                                                                                 L2-FEB-1999;
                         04-DEC-2000
                                                                                                                                     Homo sapiens
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  AAB08261;
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Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL-- 145
                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a human cytokine, designated THANK. THANK is a tumour necrosis factor (TNF) homologue that activates apoptosis, nuclear factor-kB, and c-jun N-terminal kinase. Inhibitors of the THANK polypeptide are used to inhibit the activation of nuclear factor-kB in cells. The method is used to inhibit the activation of nuclear factor-kB in cells, treat pathological conditions such as toxic and septic shock, acute phase response, viral infection, radiation susceptibility, atherosclerosis, cancer, acute inflammatory conditions, arthritis, allery, and graft versus host reaction, and inhibit growth of tumour cells such as myeloid cells, colon cancer cells, prostate cancer cells, cevical carcinoma cells, chronic myeloid leukemic cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                              Inhibiting the activation of nuclear factor-kB in cells for treating pathological conditions comprises treating cells with a tumour necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 KENKILVKETGYPPIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --KIFEPPAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21; Length 285;
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Pred. No. 1.1e-103;
0; Mismatches 0;
                                                                                   /note= "extracellular domain"
             "intracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGA
                                           78..111
'note= "extracellular
                                   "transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and acute myeloid leukemic cells.
                                                                                                                                                                                                                                                                                                                                Example 1; Fig 1; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.4%;
                                                                                                                                                           02-FEB-2000; 2000WO-US02751
                                                                                                                                                                                                                                                                                                      factor homolog inhibitor -
                                                                     ..285
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Best Local Similarity 76.5
Matches 218; Conservative
 1..46
/note=
                      47..77
/note=
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                                                                                                         WO200045836-A1
                                                                                                                                                                                   02-FEB-1999;
                                                                                                                                  10-AUG-2000
                                                                                                                                                                                                                                   Aggarwal BB
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The present sequence represents a human AGP-3 polypeptide. AGP-3 is a tunour necrosis factor (TNF) ligand family member. AGP-3 is a type II transmembrane protein, and is a potent B cell stimulatory factor. Expression of AGP-3 correlates to increases in the number of B cells and immunoslobulins produced. AGP-3 proteins, antibodies, and nucleic acids may be used to treat inflammatory and immune disorders, and nucleic e.g. rheumatoid arthritis, Crohn's disease, lupus and graft versus host disease. The nucleic acids may be used to regulate the expression of an AGP-3 related protein. The AGP-3 proteins, antibodies and nucleic ands are also useful for the detection of AGP-3 agonists, antagonists and characterizing interactions with AGP-3 related proteins.

Contact this sequence is not specifically claimed. It is only mentioned in the claims, in that a polypeptide that does not comprise the present expression in that a polypeptide that does not comprise the present in the claims.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL-- 145
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                                                                                                                                                                                                                                                                                                                                        Novel polypeptides comprising tumour necrosis factor ligand family proteins, useful for treating inflammatory and immune disorders, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.4%; Score 1042.5; DB 21; Length 285; 76.5%; Pred. No. 1.1e-103; tive 0; Mismatches 0; Indels 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 LIVVSFYQVAALQGDLASLRAELQGHHAEKLPAGA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Fig 1; 71pp; English.
99US-0166271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              rheumatoid arthritis -
                                                                                                                                                                                                                          WPI; 2000-558217/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              285 AA;
                                                                          (AMGE-) AMGEN INC.
                                                                                                                                                    Boyle WJ, Hsu H;
                                                                                                                                                                                                                                                                  N-PSDB; AAA63941
18-NOV-1999;
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Matches 218;
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AAB08261 standard; Protein; 285 AA

RESULT 10 AAB08261

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181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marsters SA, · Pitti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological activity, for treating autoimmune disorders and cancer, comprises exposing the cells to TALL-1 or APRIL polypeptide agonists or
                                                                                                                                                                                                                                                                                                                      Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
autoimmune disease; rheumatoid arthritis; multiple sclerosis;
                                                                                                     ------LEEGDELQLAIPRENAQISLDGDVTFFGALKLL 218
                                                                                                                      241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grewal I, Kim KJ,
                                                                                                                                                                                                       AAE09242 standard; Protein; 285 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-NOV-2000; 2000WO-US32378
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22-AUG-2000; 2000US-0226986.
                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                         Human TALL-1 protein.
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N-PSDB; AAD15903.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is human tumor necrosis factor (TNF)-delta protein. The TNF-delta polynucleotide is useful in gene therapy for modulating TNF-delta. TNF-delta is useful for treating deficiencies of TNF-delta and diseases ameliorated by TNF-delta. TNF-delta is also useful for screening, diagnosing, prognosing, staging or monitoring conditions or diseases attributable to TNF-delta, e.g. inflammation (e.g. inflammatory bowel disease, sepsis or rheumatoid arthritis). The TNF-delta is also useful as an anti-cancer agent to induce apoptosis in cancer and tumour-associated cells.
                                                                                                                                                                                                                                                                                                                                                                         Human; tumour necrosis factor; TNF-delta; gene therapy; antirheumatic; apoptosis; rheumatoid arthritis; cytostatic; sepsis; anti-inflammatory; inflammatory bowel disease; immunosuppressive; antiarthritic; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New tumor necrosis factors (TNF)-delta polynucleotide and polypeptide, useful in gene therapy, particularly for treating inflammation, and for inducing apoptosis in cancer and tumor-associated cells to treat cancer
                     GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE
                                                                 -----YGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQN----
 GEGNSSONSRNKRAVOGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 285;
                                                                                                                              218
                                                                                                                                                              285
                                                                                                                                                 241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL
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                                                                                                                                                                                                                                                                                                                                            Human tumour necrosis factor (TNF)-delta protein.
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Pred. No. 1.1e-103;
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                                                                                                                                                                                                                                               AAE07156 standard; Protein; 285
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76.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                             antibacterial; cancer.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2001010925-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (WILE/) WILEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-AUG-2001.
                                                                                                                                                                                                                                                                                                            06-NOV-2001
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 88
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4

67; Gaps

Score 1042.5; DB 22; Length 285; Pred. No. 1.1e-103; 0; Mismatches 0; Indels 67:

Query Match
Best Local Similarity 76.5%;
Matches 218; Conservative

44

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1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSV---

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                                                                                           GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL-- 145
                                                                                                                                                                                -----YGOVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQN---- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; tumour necrosis factor; TNF; APBF; APRIL; BAFF; therapy; melanoma; immune system-related disorder; cancer; renal cell; breast; stomach; rectal, colon; throat; bladder; ovarian carcinoma; cellular disorder; gastraintestinal; scleroderma; Kaposi's sarcoma; chronic laukaemia; squamous cell carcinoma; Hyperproliferative condition; pannus formation; shumantoid arthritis; postsurgical scarring; fibrosis; liver; uterine; lung; immunodeficiency; inflammatory disease; lymphadenopathy; vulnerary; autoimmune disease; graft versus host disease; dermatological;
                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New heteromeric ligand of tumor necrosis factor (TNF) family, useful for diagnosis, treatment of immune system-related disorders in humans, comprises TNF-family member APRIL subunit linked non-covalently to TNF-family member BAFF subunit -
                                       GEGNSSQNSRNKRAVQGPESTVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE
                                                                                                                                                                                                   181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL
                                                                              --KIFEPPAP
 Gaps
 67;
                                                                                                                                                                                                                                                     ------LEEGDELQLAIPRENAQISLDGDVTFFGALKLL 218
 Indels
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                        MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiinflammatory; immunosuppressive; cytostatic.
                                                                            LTVVSFYQVAALQGDLASLRAELOGHHAEKLPAGA
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/label= Intracellular_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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 Conservative
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N-PSDB; AAD14417.
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                                                                                                                                                                                                                                                                                                                                                                                                           Human BAFF protein
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Matches
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The present invention relates to an isolated heteromeric ligand of tumour necrosis factor (TNF)-family, referred to as APBF comprising a TNF-family member APBFL subunit linked non-covalently to TNF-family member BAFF subunit. APBF is useful for diagnosis or treatment of various immune system-related disorders in mammals, preferably humans. Such disorders include cancer, including cellular disorders, for e.g. renal cell cancer, Kaposi's sarcoma, chronic leukaemia, breast cancer, sarcoma, ovarian carcinoma, rectal cancer, throat cancer, melanoma, colon cancer, bladder cancer, squamous cellular hyperproliferative colon cancer, bladder cancer, squamous cellular hyperproliferative colon cancer, such as sclenderma, pannus formation in rheumatoid arthritis, postsurgical scarring and lung, liver and uterine fibrosis and immunodeficiencies, inflammatory diseases, lymphadenopathy, and immunodeficiencies, inflammatory diseases, lymphadenopathy, cancer immune diseases and graft versus host disease. APBF is also useful for producing monoclonal or polyclonal antibodies and for identifying circum, and modulators affecting bloogical function and receptors interacting circum, and modulators affecting bloogical function and receptors interacting contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        breast, prostate, cervical, tumour necrosis factor-alpha, TNF-alpha, cartilage, ear, proliferation, glucose, free fatty acid, skeletal muscle, adipocyte, A-peptide, factor VIIA, gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----YGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 285;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IndelB
                                                                                                                                                                                                                                                                                                                                                                       with APBF. The present sequence is human BAFF protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.4%; Score 1042.5; DB 22
76.5%; Pred. No. 1.1e-103;
.ive 0; Mismatches 0;
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Claim 2; Fig 2b; 42pp; English.
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99WO-US28634.
99WO-US28551.
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Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                285 AA;
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01-DEC-1999;
02-DEC-1999;
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AAY71915;
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AAY71915
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PRO polypeptides. The PRO polypeptides are useful to detect other
PRO polypeptides, to nink bloactive molecules to cells expressing
PRO polypeptides, to modulate bloidgical activities of cells expressing
PRO polypeptides, to modulate bloidgical activities of cells expressing
PRO polypeptides, and to detect the presence of mammalian lung, colon,
breast, prostate, rectal, cervical or liver tumours by comparing PRO
polypeptide expression in a cell sample to that in a control sample.
Some of the 275 sequences are also useful to stimulate the release of
tumour necrosis factor-alpha (TNF-alpha) from human blood, the
proliferation or differentiation of chondrocytes, the proliferation or
gene expression in pericyte cells, the release of proteogyycans from
cartilage, the proliferation of inner ear utricular supporting cells or
of T-lymphocytes, the release of a cytckine from peripheral blood
monocytes (PBMCs), or the proliferation of endothelial cells. Some of
the PRO polypeptides may modulate glucose or free fatty acid uptake by
skeletal muscle cells or by adipocytes, or inhibit binding of A-peptide
to factor VIIA. The PRO polypeptides can be used in assays to identify
RO polypeptides can be used to generate probes, antieense RNA/NNA,
transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
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Gao
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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93.4%; Score 1042.5; DB 22
Best Local Similarity 76.5%; Pred. No. 1.1e-103;
Matches 218; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Fig 24; 813pp; English.
                                                                                                                                                                                                                                                                                                                        2000WO-US13705.
2000WO-US14042.
2000WO-US14941.
                                                                     99WO-US30911.
99WO-US30999.
99WO-US31243.
                      99WO-US28565.
99US-0170262.
99WO-US30095.
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                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
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N-PSDB; AAS21255.
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20-MAR-2000;
21-MAR-2000;
                                                                      20-DEC-1999;
20-DEC-1999;
30-DEC-1999;
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22-FEB-2000;
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24-FEB-2000;
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                                                         16-DEC-1999
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Human, transmembrane activator and CAML interactor; TACI; tumour necrosis factor receptor; TNF; autoimmune disease; diabetes; calcium-signal modulating cyclophilin ligand; CAML; viral infection; neutrokine alpha polypeptide; TACI-Ligand; TACI-L; cytostatic; therapy; neuroprotective; antidiabetic; antivital; antiinflammatory; tumour; antiarthritic; antirheumatic; immunosuppressive; multiple sclerosis; rheumatoid arthritis; graft rejection; inflammation; cell proliferation; cell death; immunoslobulin E-mediated allergic reaction; 19E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of new interactions between tumour necrosis factor receptors (TACI) and TACI ligands to screen candidate molecules for determining agonist and antagonist interactions which are used for treating inflammation -
                   GEGNSSONSRNKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVFWLLSFKRGSALEE
                                                               -----YGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is a human tumour necrosis factor receptor (TACI)-ligand (TACI-L) protein.
TACI (Transmembrane activator and calcium-signal modulating cyclophilin ligand (CAML)-interactor) forms a complex with neutrokine
GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123..285
/label= TACI_binding_site
/note= "Bind@ with extracellular domain of TACI"
                                                                                                                                            -----LEEGDELQLAIPRENAQISLDGDVTFFGALKLL 218
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/label= Intracellular_domain
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/label= Transmembrane_domain
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/label= Extracellular_domain
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                                                                                                                                                                                                                                                                                                                                      Human TACI-ligand (TACI-L) protein.
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                                                                                                                                                                                                                                         AAY71915 standard; Protein; 285
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Gaps

0; Indels

45 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGA-------KIFEPPAP 87

1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSV--

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TACINITY Complex is useful for modulating an intracellular signalling cascade mediated by TACI/TACI-L complex. Antagonists of TACI/TACI-L complex are used to inhibit the interaction between TACI and TACI-L complex are used to inhibit the interaction between TACI and TACI-L for therapeutic purposes to treat tumour and tumour metastasis and to combat various autoimmune diseases e.g. multiple sclerosis and diabetes, as well as other disorders, such as viral infection, rheumaciod arthritis, graft rejection, and immunoglobulin (Ig) E-mediated allergic reactions and inflammation. The interaction is used to study cellular processes associated with tumour necrosis factor (TNF) receptors such as immune regulation, cell proliferation, cell death and inflammatory responses. The interaction between the extracellular region of TACI and TACI-L can be used to further develop understanding of which cell types TACI-L polypeptide (TACI-Ligand). The antagonist or agonist of 8888888888888888888888888

285 AA; Sequence

67; Gaps Score 1042.5; DB 22; Length 285; Pred. No. 1.1e-103; 0; Mismatches 0; Indels 67; 93.4%; Query Match Best Local Similarity 76.5%; Matches 218; Conservative

1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSV-

-----KIFEPPAP 87 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGA------45

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61

88 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL-- 145

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Search completed: February 3, 2004, 07:48:16 Job time : 38.3333 secs

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February 3, 2004, 07:45:42; Search time 211.218 Seconds (without alignments) 216.106 Million cell updates/sec
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1 MDDSTEREQSRLTSCLKKRE.......ENAQISLDGDVTFFGALKLL 218
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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/ptodata/2/pubpaa/US09C PUBCOMB.pep:
/ptodata/2/pubpaa/US09 NEW PUB.pep:
/ptodata/2/pubpaa/US10A PUBCOMB.pep;
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ptodata/2/pubpaa/US10B_PUBCOMB.pep.
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/cgn2 6/ptodata/2/pubpaa/US60 NEW PUB.pep:
/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 1, Appl Sequence 2, Al Sequence 4, Al Sequence 3228 Sequence 2, Ag Sequence 1, Ag Sequence 23, A Sequence 2, A Sequence 1 Sequence 24 Sequence 2 Sequence Description Sequence US-09-929-493-2 US-09-779-050A-2 US-09-302-863-4 US-09-980-748-3228 US-09-932-613-173 US-10-137-870-24 US-10-140-018-24 US-10-140-024-24 US-09-193-663-2 US-09-877-156-1 US-09-879-919-23 SUMMARIES Query Match Length DB 1042.5 1042.5 1042.5 1042.5 1042.5 1042.5 1042.5 1042.5 1042.5 1042.5 Result No.

4 Sequence 2	24,	24,	24,	e 5	24,	24,	4 Sequence 24,	4 Sequence 24,	4 Sequence 24,	4 Sequence 24,	4 Sequence 24,	24,	4 Sequence 24,	4 Sequence 24,	4 Seguence 24,	4 Seguence 24,	4 Seguence 24,	4 Seguence 24,	4 Sequence 24,	4 Seguence 24,	24,	4 Seguence 24,	24,	24,	24,	3 24,	24,	24,	e 7	
US-10-	US-10-140-	US-10-	US-10-	US-10.	US-10.	US-10-141	US-10-141-	US-10-142-421-	US-10-142-432-	US-10-142-767-	US-10-143-033-	US-10-144	US-10-145-62	US-10-145-	US-10-145-633-	US-10	US-10-145-74	US-10-145-82	US-10-145-82	US-10-145-87	US-10-145-87	US-10-14	US-10-146-7	US-10-146-7	US-10-14	US-10-147-4	US-10-147-5	US-10-147-5	US-10-147-5	
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16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

RESULT 177-1

1 GS-09-911-77-1

1 Sequence 1, Application US/09911777

2 Sequence 1. Application US/09911777

2 Patent No. US20020037852A1

3 PAPLICANT: BROGEN, INC.

4 APPLICANT: AMBROSE, Christiane

APPLICANT: AMBROSE, Christiane

APPLICANT: AMBROSE, Christiane

APPLICANT: AMBROSE, Christiane

APPLICANT: SCHNEIDER, Pablenne

APPLICANT: SCHNEIDER, Pabcal

TITLE OF INVENTION: in the Modulation of B-Cell Response

TITLE OF INVENTION: in the Modulation of B-Cell Response

TITLE OF INVENTION: in the Modulation of B-Cell Response

TITLE OF INVENTION: in 1980-107-24

TITLE OF INVENTION: UNMBER: 60/117,169

PRIOR FILING DATE: 1999-01-25

PRIOR FILING DATE: 1999-01-25

PRIOR FILING DATE: 1999-01-25

PRIOR FILING DATE: 1999-01-25

NUMBER OF SEQ ID NOS: 22

NUMBER OF SEQ ID NOS: 22

SEQ ID NO 1

LENGTH: 218

TYPE: RRT

TYPE: RRT

TYPE: RRT

TYPE: RRT

CGRANISM: Homo Sapien

Query Match 100.0%; Score 1116; DB 9; Length 218; Best Local Similarity 100.0%; Pred. No. 4.4e-114; Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps

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CORRESPONDENCE ADDRESS:
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                                                                                                                                   61 ASLRAELQGHHAEKLPAGAKIFEPPAPGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADS 120
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                                                 ASLRAELQGHHAEKLPAGAKIFEPPAPGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASLRAELOGHHAEKLPAGAKI FEPPAPGEGNSSONSRNKRAVOGPETVTODCLOLIADS
                      ASLRAELQGHHAEKLPAGAKI FEPPAPGEGNSSONSRNKRAVQGPEETVTQDCLQLIADS
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                                                                                                                                                                                                                               RCIQNLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 218
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100.0%; Pred. No. 4.4e-114;
iive 0; Mismatches 0; ]
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Publication No. US20010010925A1
GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: TNR-DELTA LIGAND AND USES
TITLE OF INVENTION:
UNMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MACKAY, Fabienne
APPLICANT: MACKAY, Fabienne
APPLICANT: MACKAY, Susan
TITLE OF INVENTION: BAFF, Inhibitors Thereof and
TITLE OF INVENTION: In the Modulation of B-Cell
TITLE OF INVENTION: Autoimmune Disorders
FILE REFERENCE: 08201.0034-01000
CURRENT FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/117,169
PRIOR FILING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: 60/143,28
PRIOR APPLICATION NUMBER: 60/143,28
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1099-07-09
PRIOR FILING DATE: 1090-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
SOFTWARE: FASTESC for Windows Version 4.0
SEC ID NOS: 22
                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/10045574A Publication No. US20030095967A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 218, Conservative
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                 RESULT 2
US-10-045-574A-1
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US-08-971-317A-2
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61 LIVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120
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TITLE OF INVENTION: TWP-DELTA LIGAND AND USES THEREOF
FILE REFERENCE: 6255.US.02
CURRENT APPLICATION NUMBER: US/09/193,663
CURRENT FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: 60/065,916
EARLIER FILING DATE: 1997-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 8;
                                                                                                                                                     ZUMATER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: BISH Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTESO for Windows
SOFTWARE: FASTESO for Windows
VERENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,317A
APPLICATION NUMBER: US/08/971,317A
APPLICATION NUMBER:
FILING DATE:
ATTOMNEY AGENT INFORMATION:
NAME: GOller, Mimi C
REGISTRATION NUMBER:
NAME: GOLLER, Mimi C
REGISTRATION NUMBER:
REGISTRATION NUMBER: 39,046
REGISTRATION NUMBER: 39,046
REGISTRATION NUMBER: 6255.US.01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSV-
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Abbott Laboratories
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                            100 Abbott Park Road
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TYPE: amino acid
STRANDEDNESS: single
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Matches 218; Conservative
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SEQUENCE CHARACTERISTICS
LENGTH: 285 amino acid
              STREET: 100 ...
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US-08-971-317A-2
                                                                                                STATE: II COUNTRY:
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Patent No. US20020055625A1
GENERAL INFORMATION:
APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
FILE REPERENCE: 1408.0031/20130.439C1
CURRENT APPLICATION NUMBER: US/09/877,156
CURRENT FILING DATE: 2001-06-08
PRIOR FILING DATE: 1998-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 285
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Pred. No. 7.7e-106;
0; Mismatches 0;
                                                                                                                           Query Match
93.4%; Score 1042.5; DB 9
Best Local Similarity 76.5%; Pred. No. 7.7e-106;
Matches 218; Conservative 0; Mismatches 0;
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NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 285
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76.5%;
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Best Local Similarity 76.5
Matches 218; Conservative
                                                            TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: human
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88 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL-- 145
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Patent No. US20020115112A1
GENERAL INFORMATION:
APPLICANT: Yu et al.
TITLE OF INVENTION: Neutrokine-alpha and Neutrokine-alpha Splice Variant
FILE REFERENCE: PF943P4
CURRENT APPLICATION NUMBER: US/09/929,493
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GENERAL INFORMATION:

TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
FILE REFERENCE: PPESSP1

CURRENT APPLICATION NUMBER: US/09/879,919

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: 60/277,978

PRIOR APPLICATION NUMBER: 60/277,978

PRIOR APPLICATION NUMBER: 60/277,978

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR PILING DATE: 2001-03-23

PRIOR PELING DATE: 2000-10-23

PRIOR PELING DATE: 2000-12-13

PRIOR APPLICATION NUMBER: 60/241,952

PRIOR APPLICATION NUMBER: 60/241,952

PRIOR PILING DATE: 2000-16-23

PRIOR PILING DATE: 2000-16-33

PRIOR PILING DATE: 2000-16-33

PRIOR PILING DATE: 1997-03-12

PRIOR PILING DATE: 1997-03-12

PRIOR FILING DATE: 1997-03-14

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin Ver: 2.1
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Pred. No. 7.7e-106;
0; Mismatches 0;
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Patent No. US20020064829A1
GENERAL INFORMATION:
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93.4%;
Best Local Similarity 76.5%;
Matches 218; Conservative
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US-09-879-919-23
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Pred. No. 7.7e-106;
0; Mismatches 0;
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Patent No. US20020160416A1
GENERAL INFORMATION:
APPLICANT: BOYLE, WILLIAM
APPLICANT: HSU, HAILING
ITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
FILE REFERENCE: A-570B
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 06/181,800
PRIOR APPLICATION NUMBER: 60/181,800
PRIOR PLING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 285
             PRIOR APPLICATION NUMBER: 60/22, 628
PRIOR FILING DATE: 2000-08-15
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-23
PRIOR PILING DATE: 2000-09-23
PRIOR APPLICATION NUMBER: 60/234, 338
PRIOR PILING DATE: 2000-09-22
PRIOR PILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-03-06
PRIOR PILING DATE: 2001-03-06
PRIOR PILING DATE: 2001-03-06
PRIOR PILING DATE: 2001-03-06
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-06-07
PRIOR PILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 47
 2001-08-15
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Best Local Similarity 76.5%;
Matches 218; Conservative
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; ORGANISM: Homo sapiens
US-09-929-493-2
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; ORGANISM: Homo sapiens
US-09-779-050A-2
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US-09-779-050A-2
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88 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL-- 145
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                                                                                                          ---KIFEPPAP
                                                                                                                                                                                                                                                                                                                                        146 -----YGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQN----
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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APPLICANT: GOODWIN, WANWAN S.
TITLE OF INVENTION METHODS OF USE OF THE TACI/TACI-L INTERACTION
FILE REFERENCE: 2519
CURRENT APPLICATION NUMBER: US/09/302,863
CURRENT FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
    Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                              241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
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    DB 10;
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                                                                                      1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSV-
Score 1042.5; DB 1:
Pred. No. 7.7e-106;
0; Mismatches 0;
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10S-09-880-748-3228
; Sequence 3228, Application US/09880748
; Publication No. US20030059937A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09302863; Publication No. US20030022233A1; GENERAL INFORMATION:
    93.4%;
                         Best Local Similarity 76.5
Matches 218; Conservative
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US-09-302-863-4
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Best Local
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Matches 218; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REPERENCE: Dyx-025.1 PCT, DXX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT PILING DATE: 2001-08-17
                APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERRECE: FF23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11; Length 285,
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Pred. No. 7.7e-106;
0; Mismatches 0;
                                                               CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PLICATION NUMBER: 60/277,379
PRIOR PLICATION NUMBER: 60/277,379
PRIOR PLICATION NUMBER: 60/293,499
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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Publication No. US20030091565A1
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SOFTWARE: Patentin version 3.1
SEQ ID NO 173
LENGTH: 285
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Matches 218, Conservative
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CORGANISM: Homo sapiens
US-09-880-748-3228
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ORGANISM: Homo Sapiens
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Score 1042.5; DB 11; Length 285; Pred. No. 7.7e-106;

93.4%; 76.5%;

Query Match Best Local Similarity

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145
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                                                                               1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P33304018 NUMBER: US/10/137,870
CURRENT APPLICATION NUMBER: US/10/137,870
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    Indels
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Pred. No. 7.7e-106;
0; Mismatches 0;
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    Mismatches
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76.5%;
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DeForge, Laura
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Filvaroff, Ellen
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Godowski, Paul J
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Best Local
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APPLICANT
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                   1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 60
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330HGLTS G
CURRENT APPLICATION NUMBER: 10/10/140,018
CURRENT FILING DATE: 2002-05-06
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                                                                                    241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285
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Pred. No. 7.7e-106;
0; Mismatches 0;
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                                                                                                                                                                                  Sequence 24, Application US/10140018
Publication No. US20030138885A1
GENERAL INFORMATION:
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Best Local Similarity 76.5%;
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          Smith, Victoria
Stewart, Timothy A
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Wood, William
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Gurney, Austin L.
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Filvaroff, Ellen
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; ORGANISM: Homo Sapien
US-10-140-018-24
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US-10-140-018-24
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RESULT 14 US-10-140-021-24 ; Sequence 24, Application US/10140021

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND THE SAME
TITLE OF INVENTION: ACCOUNT THE SAME
FILE REPERENCE: P3330R1C167
CURRENT APPLICATION NUMBER: US/10/140,021
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 GEGNSSONSRNKRAVOGPEETVTQDCLQLIADSETPTIOKGSYTFVPWLLSFKRGSAL--
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76.5%; Pred. No. 7.7e-106;
tive 0; Mismatches 0;
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Publication No. US20030138886A1
                                                                                                                                                                                                                                                                                                              Stewart, Timothy A
                                                                                                                                                                               Gerritsen, Mary E.
                                         Baker, Kevin P.
Beresini, Maureen
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Wood, William
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Gurney, Austin L.
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Gurney,Austin L.
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Smith, Victoria
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Filvaroff, Ellen
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Best Local Similarity 76.5
Matches 218; Conservative
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                                                                                       DeForge, Laura
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US-10-140-021-24
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APPLICANT:
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67; Gaps . '4;
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                APPLICANT: Tummas, Daniel
APPLICANT: Wasdanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C161
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Pred. No. 7.7e-106;
0; Mismatches 0; Indels
                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/140,274
CURRENT FILING DATE: 2002-05-06
Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
LENGTH: 285
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ewart, Timothy A.
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Best Local Similarity 76.5
Matches 218; Conservative
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CORGANISM: Homo Sapien
US-10-140-274-24
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Search completed: February 3, 2004, 08:02:16 Job time : 212.218 secs

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Sequence 4, Apple Sequence 164, App Sequence 164, App Sequence 2, Appli

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Sequence 3

Sequence

Sequence 3 Sequence 2 Sequence 2

Sequence Sequence Sequence Sequence

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GEGNSSONSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
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Batent No. 6297367
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLS OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/286,529
CURRENT FILING DATE: 1999-04-05
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL
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Pred. No. 5.4e-118;
; Mismatches 0;
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US-09-879-919-11

US-09-157-864-2

US-09-879-919-13

US-10-082-260-4

US-09-879-919-4

US-09-879-919-4

US-09-889-2878-20

US-09-588-2878-20

US-09-588-2878-20

US-09-496-1188-3

US-09-496-1188-4

US-09-496-1188-4

US-09-496-1188-4

US-09-496-1188-4

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US-09-300-909-20

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76.5%;
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Best Local Similarity 76.5
Matches 218; Conservative
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CRGANISM: human
US-09-286-529-1
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Compugen Ltd
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US-09-5879-919-23
US-09-589-947A-2
US-09-589-947A-2
US-09-589-947A-19
US-09-588-947A-19
US-09-588-947A-28
US-09-588-947A-30
US-09-588-947A-38
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-09-496-118B-2
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                   GenCore version (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1 MDDSTEREQSRLTSCLKKRE.
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seq length: 200000000
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Post-processing:

Database

Minimum DB Maximum DB

score:

Title: Perfect :

Run on:

Sequence:

Scoring table:

Searched:

9

Gaps

67;

Indels

1042.5 1042.5 1042.5 1042.5 1042.5 1042.5

Result Š. Sequence 2, Application US/09589287B
Patent No. 640370
GENERAL INFORMATION:
TITLE OF INVENTION: Antibodies to Neutrokine-alpha

RESULT 2 US-09-589-287B-2

Sequence

927 927 927 773.5 773.5 773.5 773.5 83.1 823.5 823.5 83.7 152 152 152 150 150 150

Sequence Sequence

Sequence Sequence

JS-09-153-927-.08-815-783-

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121 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
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; Sequence 23, Application US/09879919
; Patent No. 6541224
; GENERAL INFORMATION:
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Best Local Similarity 76.55
Matches 218; Conservative
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SOFTWARE: Patentin Ver. 2
SEQ ID NO 2
LENGTH: 285
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                                                                                                                                                                                                                                                       67; Gaps
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TILLE OF INVENTION: Uses of THANK, a TNF homologue that Activates TITLE OF INVENTION: Apoptosis FILE REFERENCE: D6206 CURRENT EPERENCE: D6206 CURRENT APPLICATION NUMBER: US/09/496,118B PRIOR APPLICATION NUMBER: US 60/118,531 PRIOR FILING DATE: US 60/118,531 NUMBER: OF SEQ ID NOS: 13
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93.4%; Score 1042.5; DB 4; Length 285;
Best Local Similarity 76.5%; Pred. No. 5.4e-118;
Matches 218; Conservative 0; Mismatches 0; Indels 67;
                                                                                                                                                                                                                    Length 285;
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FILE REFERENCE: PF343P3C1
CURRENT APPLICATION NUMBER: US/09/589,287B
CURRENT FILING DATE: 2000-06-08
CURRENT FILING DATE: 2000-06-08
Prior application data removed - check PALM or file wrapper NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
LENGTH: 285
                                                                                                                                                                                                                                                       Indels
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Pred. No. 5.4e-118;
                                                                                                                                                                                                                                                       0; Mismatches
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Patent No. 6475986
GENERAL INFORMATION:
APPLICANT: Aggarwal, Bharat B.
                                                                                                                                                                                                                    93.4%;
76.5%;
                                                                                                                                                                                                                                    Best Local Similarity 76.5
Matches 218, Conservative
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                                                                                                                                              TYPE: PRT
ORGANISM: human
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US-09-496-118B-1
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Sequence 2. Application US/09565423

Patent No. 6475997

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 2879-72

CURRENT APPLICATION NUMBER: US/09/565,423

CURRENT FILING DATE: 2000-05-05

PRIOR APPLICATION NUMBER: 60/132,892

PRIOR FILING DATE: 1999-05-06
181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240
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TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
CURRENT PELICATION HUMBER: US/09/879,919
CURRENT APPLICATION NUMBER: 60/293,499
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.4%; Score 1042.5; DB 4; Length 285; 76.5%; Pred. No. 5.4e-118;
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US-09-565-423-2
                                                                 218
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0; Mismatches 0;
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93.4%; Score 1042.5; DB 4
76.5%; Pred. No. 5.4e-118;
ive 0; Mismatches 0;
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TITLE OF INVENTION: Antibodies to Neutrokine-alpha FILE REFERENCE: PF343B3C1
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PRIOR APPLICATION NUMBER: 60/131,278
PRIOR PILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131,673
PRIOR PILING DATE: 1999-04-29
PRIOR PILING DATE: 1999-04-29
PRIOR PILING DATE: 1999-04-29
PRIOR PELING DATE: 1999-07-06
PRIOR PILING DATE: 1999-07-06
PRIOR PILING DATE: 1999-07-06
PRIOR PILING DATE: 1999-07-06
PRIOR PILING DATE: 1999-11-24
PRIOR PELICATION NUMBER: 60/167,239
PRIOR PELING DATE: 1999-11-24
PRIOR PELING DATE: 1999-12-03
PRIOR PELING DATE: 1999-12-03
PRIOR PELING DATE: 1999-12-04
PRIOR PELING DATE: 1999-12-16
PRIOR PELING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/171,626
PRIOR PELING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/16,015
PRIOR PELING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 09/255,794
PRIOR PILING DATE: 1999-0-13
PRIOR PELING DATE: 1999-0-13
PRIOR PELING DATE: 1998-0-1-12
PRIOR PELING DATE: 1998-0-1-12
PRIOR PELING DATE: 1998-0-1-12
PRIOR PELING DATE: 1998-0-1-12
PRIOR PELING DATE: 1998-0-1-14
PRIOR PILING DATE: 1998-0-1-14
PRIOR FILING DATE: 1998-0-1-15
PRIOR PELING DATE: 1998-0-1-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 93.4
Best Local Similarity 76.5
Matches 218; Conservative
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; ORGANISM: human
US-09-588-947A-2
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GENERAL INFORMATION:
APPLICANT: Yu et al.
TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokine-alpha
FILE REPREBRENCE: PF243782
CURRENT APPLICATION NUMBER: 09/588,947A
CURRENT PILING DATE: 2000-06-08
FRIOR PELING DATE: 2000-06-08
FRIOR PELING DATE: 2000-06-08
FRIOR PELING DATE: 2000-02-22
FRIOR PELING DATE: 1999-03-22
FRIOR PELING DATE: 1999-03-22
FRIOR PELING DATE: 1999-03-02
FRIOR PELING DATE: 1999-03-04
FRIOR PELING DATE: 1999-03-05
FRIOR FILING DATE: 1999-03-05
FRIOR FILING DATE: 1999-03-05
FRIOR PELING DATE: 1999-04-02
FRIOR PELING DATE: 1999-04-16
FRIOR PELING DATE: 1999-04-16
FRIOR PELING DATE: 1999-04-16
FRIOR PELING DATE: 1999-04-16
FRIOR FILING DATE: 1999-04-16
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Pred. No. 5.4e-118;
0; Mismatches 0;
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                              PRIOR FILING DATE: 2001-03-23
PRIOR PILING DATE: 2001-03-6,248
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2000-13-16
PRIOR PILING DATE: 2000-12-13
PRIOR PILING DATE: 2000-12-13
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 1990-06-15
PRIOR PILING DATE: 1997-03-12
PRIOR PILING DATE: 1996-03-14
NUMBER OF SEQ ID NOS: 26
SEG ID NO 23
LENGTH: 285
            APPLICATION NUMBER: 60/277,978
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Sequence 2, Application US/09588947A;
Patent No. 6562579
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Best Local Similarity 76.5%;
Matches 218; Conservative
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; ORGANISM: Homo sapiens
US-09-879-919-23
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61 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAP 120 121 GEGNSSONSRNKRAVOGPBETVTODCLOLIADSETPTIOKGSYTFVPWLLSFKRGSALEE 180 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 240 ---KIFEPPAP 87 1 MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCC 88 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL--DB 4; Length 285; 218 241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 285 CURRENT APPLICATION NUMBER: US/09/589,287B
CURRENT FILING DATE: 2000-06-08
Prior application data removed - check PALM or file wrapper NUMBER OF SEQ ID NOS: 42

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45 LTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGA---
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NUMBER OF SEQ ID NOS: 42
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GENERAL INVENTALION:

TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
FILE REPREBRENCE: PF533P1
CURRENT APPLICATION NUMBER: US/09/879,919
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-03-23
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR PRIOR PAPLICATION NUMBER: 60/274,875
PRIOR APPLICATION NUMBER: 60/244,875
PRIOR FILING DATE: 2000-12-13
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 1990-03-12
PRIOR FILING DATE: 1996-03-14
NUMBER OF SEQ ID NOS: 26
SOUTHWARE: BALCH NUMBER: 60/211,537
PRIOR FILING DATE: 1996-03-14
NUMBER OF SEQ ID NOS: 26
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                                                                                                                                 Length 266;
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Pred. No. 5e-104;
0; Mismatches
                                                                                                                                                  Pred. No. 5e-1
0; Mismatches
                                                                                                                         Query Match 83.1%; Score 927;
Best Local Similarity 69.8%; Pred. No. 5
Matches 199; Conservative 0; Mismatch
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69.8%;
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 69.8
Matches 199; Conservative
                                                  TYPE: PRT
ORGANISM: Homo sapiens
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CRGANISM: Homo sapiens
US-09-879-919-24
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                 SEQ ID NO 19
LENGTH: 266
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APPLICANT: Yu et al.

TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokine-alpha FILE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokine-alpha FILE OF INVENTION: PF343P302
CURRENT APPLICATION WUMBER: US/09/588,947
PRIOR APPLICATION WUMBER: 09/589,947
PRIOR PLING DATE: 2000-06-08
PRIOR FILING DATE: 2000-06-08
PRIOR FILING DATE: 2000-02-22
PRIOR PLING DATE: 1099-03-02
                                                                                                                                                                                                                                                    162 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETL 221
------GSYTFVPWLLSFKRGSALEE
                                                                           88 GEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL--
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                                                                                                                            121 GEGNSSQNSRNKRAVQGPEET-----
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APPLICATION NUMBER: PCT/US96/17957
FILING DATE: 1996-10-25
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RIOR APPLICATION NUMBER: 60/136,784
REAR FILING DATE: 1999-05-28
RIOR APPLICATION NUMBER: 60/142,659
RIOR APPLICATION NUMBER: 60/142,659
RIOR PILING DATE: 1999-07-06
RRIOR APPLICATION NUMBER: 60/145,824
RRIOR APPLICATION NUMBER: 60/145,824
RRIOR APPLICATION NUMBER: 60/167,239
RRIOR FILING DATE: 1999-07-7
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PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/127,598
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: 60/130,412
PRIOR FILING DATE: 1999-04-16
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PRIOR FILING DATE: 1999-04-23
PRIOR APPLICATION NUMBER: 60/131,278
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131,673
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PRIOR APPLICATION NUMBER: 60/171,626
PRIOR FILING DATE: 1999-12-23
PRIOR PELICATION NUMBER: 60/176,015
PRIOR FILING DATE: 2000-01-14
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Patent No. 6562579
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PRIOR FILING DATE: 1999-03-12
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APPLICATION NUMBER: 60/130,696
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APPLICATION NUMBER: 60/168,624
FILING DATE: 1999-12-03
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PRIOR FILING DATE: 1999-022-23
PRIOR APPLICATION NUMBER: 09/005,874
PRIOR FILING DATE: 1998-01-12
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APPLICATION NUMBER: 60/131,673
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Sequence 28, Application US/09588947A
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                                                                                                     83.1%; Score 927; DB 4; Length 266; 69.8%; Pred. No. 5e-104;
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                                                                                                                                   0; Mismatches
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 266
                                                                                                                   Best Local Similarity 69.8
Matches 199; Conservative
                                           TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 162; Conserv
                                                                        US-09-588-947A-19
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Sequence 30, Application US/09588947A
Fatent No. 656279
GENERAL INFORMATION:
APPLICANT: Yu et al.
TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokine-alpha
FILE REFERENCE: PF342P3C2
CURRENT FILING DATE: 2000-06-08
FRIOR FILING DATE: 2000-06-08
FRIOR APPLICATION NUMBER: 09/588,947
FRIOR PILING DATE: 2000-06-08
FRIOR APPLICATION NUMBER: 09/507,968
FRIOR PELING DATE: 1999-03-02
FRIOR FILING DATE: 1999-03-02
FRIOR FILING DATE: 1999-03-12
FRIOR FILING DATE: 1999-03-16
FRIOR FILING DATE: 1999-03-16
FRIOR FILING DATE: 1999-04-02
FRIOR FILING DATE: 1999-04-02
FRIOR FILING DATE: 1999-04-02
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                          121 VKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCY 180
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----YGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQN--
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 219
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                                                                                       186 -----LEEGDELQLAIPRENAQISLDGDVTFFGALKLL 218
                                                                                                                                                                                                                                                                     Parent No. 6403770
GENERAL INFORMATION:
APPLICANT: Yu et al.
TITLE OF INVENTION:
FILE REFERENCE: PF343P3C1
CURRENT APPLICATION NUMBER: US/09/589,287B
CURRENT FILING DATE: 2000-06-08
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US-09-589-287B-30
; Sequence 30, Application US/09589287B
nreat No. 6403770
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Matches 161; Conservative
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CORGANISM: Homo sapiens
US-09-589-2878-30
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Patent No. 6475986
Patent No. 6475986
TEREAL INFORMATION: Uses of THANK, a TNF homologue that Activates TITLE OF INVENTION: Uses of THANK, a TNF homologue that Activates TITLE OF INVENTION: Apoptosis
TITLE OF INVENTION: Apoptosis
TITLE OF INVENTION: Apoptosis
TITLE OF INVENTION APPLICATION NUMBER: US/09/496,118B
CURRENT APPLICATION NUMBER: US 60/118,531
PRIOR APPLICATION NUMBER: US 60/118,531
NUMBER OF SEQ ID NOS: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 773.5; DB 4; Length 219;
Pred. No. 1.6e-85;
3; Mismatches 4; Indels 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 -----YGOVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 -----LEEGDELQLAIPRENAQISLDGDVTFFGALKLL 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 SAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 219
PRIOR APPLICATION NUMBER: 60/131,278
PRIOR APPLICATION NUMBER: 60/131,673
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1999-07-06
PRIOR FILING DATE: 1999-07-06
PRIOR PLING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-27
PRIOR PLING DATE: 1999-10-24
PRIOR PILING DATE: 1999-11-24
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-01-14
PRIOR PILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-13
PRIOR FILING DATE: 1996-10-25
NUMBER: OF 0036, 100
PRIOR FILING DATE: 1996-10-25
NUMBER: OF 0036, 100
PRIOR FILING DATE: 1996-10-25
PRIOR FILING DATE: 1996-10-25
NUMBER: OF 0036, 100
PRIOR FILING DATE: 1996-10-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.3%;
73.5%;
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Best Local Similarity 73.5
Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-588-947A-30
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62 KRGSALEEKENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRC 121
                                                                                                                                                                                                                                                                     80 KIFEPPAPGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSF 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 YTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQN------LEEGDELQ 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKILVKETGYFFIYGQVL 60
                                                                                                                                                                                                                                                                                            2 KIFEPPAPGEGNSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWILSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels 34; Gaps
                                                                                                                                                                                                                              34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 IQNMPETLPNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL 174
                                                                                                                                                                              Score 681; DB 4; Length 174;
Pred. No. 1.9e-74;
0; Mismatches 0; Indels 3
TYPE: PRT
CRGANICH: Homo sapiens
FEATURE:
NAME/KEY: domain
COCATION: 112.285
OTHER INFORMATION: sequence of THANK extracellular domain
US-09-496-118B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INCORMATION:
APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MENBERS OF THR AND THER FAMILIES
FILE REFERENCE: 11408.003.7200130.439C1
CURRENT APPLICATION NUMBER: US/09/286,529
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 TVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 47.8%; Score 533; DB 3;
Best Local Similarity 76.6%; Pred. No. 1.3e-56;
Matches 111; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: February 3, 2004, 07:44:54 Job time: 16.0489 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 LAIPRENAQISLDGDVTFFGALKLL 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21, Application US/09286529 Patent No. 6297367
                                                                                                                                                                              Query Match
Best Local Similarity 80.3%;
Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Homo sapien
US-09-286-529-21
                                                                                                                                                                                                                                                                                                                                                          140 KRGSAL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 IQN
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SEQ ID NO 21
LENGTH: 145
TYPE: PRT
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WASH WANTE TOWN SHILL

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GenCore version 5.1.6
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OM protein - protein search, using sw model

February 3, 2004, 07:43:37; Search time 14.4356 Seconds (without alignments) 1545.568 Million cell updates/sec Run on:

US-09-911-777-2 Title: Perfect score;

1204 1 MDESAKTLPPPCLCFCSEKG.....ENAQISRNGDDTFFGALKLL 232 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

probable tRNA pyro	probable nucleic-a	conserved hypothet	hypothetical prote	hypothetical prote	tryptophan synthas	hypothetical prote	sensor protein kin	toxin secretion AB	hypothetical prote	exodeoxyribonuclea	transforming prote	hypothetical prote	yes-associated pro	sensor histidine k	protein F1504.11 [
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A71473	A97292	T39641	E96642	H69935	S26665	T33131	D86750	AH2335	T23001	F83110	TVHUL2	T15966	150730	A75481	D86478
7	~	~	7	~	~	~	~	~	~	~	н	0	~	~	~ ′
339	357	547	1188	297	346	365	441	1003	430	1171	357	428	448	995	1465
6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.2	6.2	6.2	6.2	6.2	6.2	6.2
92	9/	16	94	75.5	75.5	75.5	75.5	75.5	75	75	74.5	74.5	74.5	74.5	74.5
30	31	32	33	34	32	36	37	38	39	40	41	42	. 43	44	45

ALIGNMENTS

RESULT 1 151083 SOX-LZ - rainbow tr. C;Species: Oncorhyn C;Date: 13-Sep-1996 C;Accession: 151083 Mol. Cell. Biol. 15 A;Title: A gene tha A;Reference number: A;Accession: 151083 A;Status: prelimina A;Rolecule type: mR A;Residues: 1-767 A;Residues: 1-767 A;Cross.references: C;Superfamily: HMG F;554-629/Domain: H	RESULT 1 151083 SOX-LG - rainbow trout C;Species: Oncorhynchus mykiss (rainbow trout) C;Accession: I51083 C;Accession: I51083 Mol. Cell. Biol. 15, 3759-3766, 1995 Mol. Cell. Biol. 15, 3759-3766, 1995 A;Title: A gene that is related to SRY and is expressed in the testes encodes a leucine A;Reference number: I51083; MUID:95311974; PMID:7791783 A;Reference number: I51083 A;Reference number: I51083 A;Residues: 1-767 cranslated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-767 crans A;Residues: I-767 crans C;Superferences: GB:D61688; NID:9927216; PIDN:BAA09617.1; PID:9927217 F;S54-629/Domain: HMG box homology cHMGl>
Query Match Best Local Matches 5	Query Match 7.1%; Score 85; DB 2; Length 767; Best Local Similarity 22.0%; Pred. No. 12; Matches 52; Conservative 40; Mismatches 86; Indels 58; Gaps 11;
λo qa	10 PPCLCFCSEKGEDMKVGYDPITPQKEEGAVLLSSSFTAMSLYQLAALQADLMNLRMELQS 69
oy, Db	70 YRGSATPAAAKLITPAAPRPHNSSRGHRNRRAFPGPEETEQDVDLSAPPA 119
o o o	120 LRNIIQDCLQLIADSDTPTIRKGTYTFVPWLLSFKRGNALYSQVLYTDPIFAMGH 174 :::
δ	175 -VIORKKVHVFGDELSLVTLFRCIONLEEGDEIQLAIPRENAQISRNGDDTFFGAL 229

A70646

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Cipate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
Cipate: 17-Jul-1998 #sequence_revision 17-Jul-1998
Cipate: 17-Jul-1998

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nematode C. elegans: a platform for investigating biolog
                                                                                                                                                                                                                                                                                                                                                     51; Conservative
                                                                                                                                                              A; Residues: 1-1121 <STO>
                                                                                                                                                                                                                                                                                                                             Similarity
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A;Molecule type: DNA
                                                                                                                                           Molecule type: DNA
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                                                                                                                                                                                                            Genetics:
Gene: Y43F8C.12
                                                                                                                                                                                                                                                          A; Map position:
                                                                                                                                                                                                                                                                                                     Query Match
Best Local S:
Matches 51
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;Status: preliminary; nucleic acid sequence not shown; translation not shown; Molecule type: DNA;Rosidues: 1-380 <COL>;Residues: 1-380 <COL>;Cross_references: GB:Z03867; GB:AL123456; NID:G3261695; PIDN:CAB06278.1; PID:e291015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: CESP:Y43FBC.12
A;Introns: 45/3; 140/3; 270/3; 300/1; 360/2; 419/3; 677/3; 824/3; 856/3; 949/1; 1113/2
                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                           102 AMTLPPPV-------VAANRIQLLALIATNFFGONTAAIAATEAQYAEMW 144
                                                                                                                                                                                                                                                                                                                                                                         64 RMELQSYRGSAT-PAAAKLIJPAAPRPHNSSRGHRNRRAFPGPEETEQDVDLSAPPALRN 122
                                                                                                                                                                                                                                                                                                                                                                                                                         ----PRQTINPAGLIAQAAVS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      605 LRSPMTMIÄLLINQAVQAVVSNKRLK-----EFLVÄEELDEKCVDRSVNIERSHNAVR 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              658 VENLTASWDPEBAAGEKTLODVDLTAP---RNSLIAVVGKVGSGKSSLLOALLGEMGKLR 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----KGTYTFV---PWL----LSFKR--GNALYSQVLYTDPIFAMGHV----- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 GRIGVNGRVAYVPQQPWIQNMTLRDNITFGRPFDRKRYDQVLYACALKADIKILFAGDQT 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Caenorhabditis elegans
Bate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
Accession: C87973
                                                                                                                                                                                                                                                                               5 AKTLPPPCLCFCSEKGEDMKVGYDPITPQKEEGAVLLSSSFTAMSLYQLAALQADLMNL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 LSSSFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAAKLLTPAAPRPHNSSRGH----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 -RNRRAFPGPEE----TEQDVDLSAPPALRNIIQDCLQLIADSDTPTIR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 QATDPLSLLIETVTQALQALTIPSFIP------EDFTFLDAIFA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 IIQDCLOLIADSDTPTIRKGTY-TFVPWLLSFKRGNALYSQVLYTDPIFA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDN:CAA21622.2; CESP:Y43F8C.12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 1153;
                                                                                                                                                                                         Length 380;
                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                    58;
                                                                                                                                                                                         DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Reference number: 220279
A, Accession: T26883
A, Status: preliminary: translated from GB/EMBL/DDBJ
A, Molecule: preliminary: with a, Residues: 1-1153 - WILL-
A, Residues: 1-1153 - WILL-
A, Cross references: EMBL: AL032637; PIDN: CAA21622.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R, anonymous, The C. elegans Sequencing Consortium
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llarity 25.1%; Pred. No. 33;
Conservative 31; Mismatches
                                                                                                                                                                                      Query Match 7.0%; Score 84.5; Di
Best Local Similarity · 22.4%; Pred. No. 5.3;
Matches 38; Conservative 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         145 AQDAAAMYGYATASAAAALLTPFSP---
                                                                                           A, Experimental source: strain H37Rv C, Genetics: A, Gene: PPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Experimental source: clone Y43F8C C, Genetics:
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nes 60; Conserv
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Matches
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A,Reference number: A75000, MUID:99069613; PMID:9851916
A,Note: see websites genome.wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_eleA,Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A,Scession: (G7973
A,Scession: CG7973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CiDate: 12-Jul-1991 #sequence_revision 02-Jun-1994 #text_change 17-Mar-2003
CAccession: A38449; S20030; B82960
R; Wozniak, D.J.; Ohman, D.E.
J. Bacteriol. 173, 1406-1413, 1991
A; Hattle: Pseudomonas aeruginosa AlgB, a two-component response regulator of the NtrC fam A; Reference number: A38449; MUID:91139582; PMID:1899859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1.49 < MOZ.
A; Cross-references: GB: MG2902; GB: M37765; NID: 9150990; PIDN: AAA25700.1; PID: 9150991
A; Goldberg, J.B.; Dahnke, T.
Mol. Microbiol. 6, 59-66, 1992
A; Title: Pseudomona aeruginosa AlgB, which modulates the expression of alginate, is a m
A; Reference number: $20030; MUID: 92149314; PMID: 1738315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M.J.; Br
K.; Lim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A,Reference number: A82950, MUID:20437337, PMID:10984043
A,Accession: B82960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE004961; GB:AE004091; NID:g9951814; PIDN:AAG08868.1; GSPDB:GN001
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Comment: This protein is part of a two-component regulatory system for alginate biosyn Comment: Secretion of the polysaccharide alginate is responsible for mucoid colony mor
                                                                                                                                                                                                                                   A,Cross-references: GB:chr_1; PIDN:CAA21622.1; PID:g3979969; GSPDB:GN00019; CESP:Y43F8C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hickey, P
Larbig, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----KGTYTFV---PWL-----LSFKR--GNALYSQVLYTDPIFAMGHV----- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              715 GRIGVNGRVAYVPQQPWIQNWTLRDNITFGRPFDRKRYDQVLYACALKADIKILPAGDQT 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               658 VENLTASWDPEEAAGEKTLQDVDLTAP---RNSLIAVVGKVGSGKSSLLQALLGEMGKLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 LSSSFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAAKLLTPAAPRPHNSSRGH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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A;Molecule type: DNA
A;Residues: 1-449 -GQL
A;Residues: 1-449 -GQL
A;Residues: BMBL:M82823
B;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, J.; DlSON, M.V.
A;LDTY, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                     Length 1121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 -RNRRAFPGPEE----TEQDVDLSAPPALRNIIQDCLQLIADSDTPTIR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72;
                                                                                                                                                                                                                                                                                                                                                                                                     2,
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 81.5; DB Pred. No. 40; 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulatory protein algB – Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 -IQRKKVHVFGDELSLVTLFRCI-QNLE 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ::: | : | ! | | EIGEKGINLSGGOKARVSLARAVYQNLD
                                                                                                                                                                                                                                                                                                                                                                                                  6.8%; Scoi
24.5%; Prec
tive 28; N
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12;

71;

Indels

Length 1735;

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CiSpecies: Anopheles gambiae (African malaria mosquito)
CiDate: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Sep-1997
CiAccession: S27770
CiAccession: S27770
CiAccession: S27770
CiAccession: S27770
CiAccession: S27770
CiBrither Distinct families of site-specific retroposons occupy identical positions
A;Reference number: S27770
A;Accession: S27770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation elongation factor eEF-2 [similarity] - fission yeast (Schizosaccharomyces po C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 0.0-Dec-1999 #text_change 03-Nov-2000 C;Accession: T41697; T30256; T38896; T51994; T51994; T47427 R;Wedler, H.; Duesterhoeft, A.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G. A;Reference number: Z22010 A;Reference number: Z22010 A;Accession: T41697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      858 KGDDAWKVYÝDE-TAQEIVDEFAMRYGVEŠIYQÁMTHFACLSSKÝMCPGVPAVMSTĽLAN 916
                                                                                                                                                                                                                                                                                                                                                                                                                                        ----AKLLTPAAPRPHNSSR----GHRNRRAFPG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 PEETEQDV---------DLSAPPALRNIIQDCLQLIADSDTPTIRKGTYTF 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Residues: 1-1735 <RES>
A, Cross-references: BMBL:U24070; NID:g915327; PIDN:AAC52266.1; PID:g915328
C, Superfamily: protein kinase C zinc-binding repeat homology
F;567-616/Domain: protein kinase C zinc-binding repeat homology <KZ2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 SQQREEMTVPATSTPKAGKCSSAEPSLSEMNESLKLL----AMQVAQLSKELSLCRKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Genetics: SP2
R,Stevens, K.; Churcher, C.; McDougall, R.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, August 1999
A,Reference number: Z21838
                                                                                                                                                                                                                                                                                                              19 KGED-MKVGYDPITPQK--EEGAVL--LSSSFTAM-----SLYQLAALQADLMNLRME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 QADLMN---LRMELQSYRGSATPAAAKLLTPAAPRPHNSSRG---HRNRRAFPGPEETEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 SEKGEDMKV------GYDPITPQKEEGAVLLSSSFTAMSLYQLA-----AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein 1 - African malaria mosquito (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:M93690; NID:g159615; PID:g159616
                                                                                                                                                                                    6.7%; Score 80.5; DB 2;
23.3%; Pred. No. 85;
ative 26; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-842 <WED>
A;Cross-references: EMBL:AL121859; PIDN:CAB58373.1; G
A;Experimental source: strain 972h-; clone pl p31B10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
25;
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29.2%; Pred. No. 25;
ive 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 VPWLLSFKRGNALYSQVLYTDP 168
                                                                                                                                                                                    Query Match
Best Local Similarity 23.34
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 29.2
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     67 LOSYRGSATPAA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-613 <BES>
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A,Map position: 13 min

A,Map position: 13 min

S,Superfamily: response regulator of the NtrC type; response regulator homology; RNA pol

C,Superfamily: response regulator homology «RRH»

F;11-120/Domain: response regulator homology «RRH»

F;147-156/Domain: RNA polymerase sigma factor interaction domain homology «SFI»

F;175-182/Region: nucleotide-binding motif A (P-loop) #status atypical

F;42-246/Region: nucleotide-binding motif B

F;42-445/Region: helix-turn-helix motif

F;59/Binding site: phosphate (Asp) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CiSpecies: Rattus norvegicus (Norway rat)
CiDate: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
CiDate: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
CiAccession: A57607
R. Brol. Chem. 270, 25273-25280, 1995
A. Title: Mammalian homologues of Caenorhabditis elegans unc-13 gene define novel family A. Reference number: A57607, MUID: 96027639, PMID: 7559667
A. A. Recession: A57607
A. Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F19F10.10 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C.Accession: T25714
R.Kellen, J.; Wamsley, P.
Submitted to the EMBL Data Library, April 1997
A.Reference number: Z20073
A.Scorseries preliminary; translated from GB/EMBL/DDBJ
A.Status: Preliminary; translated from GB/EMBL/DDBJ
A.Residues: 1-891 <KEL>
A.Residues: 1-891 <KEL>
A.Residues: 1-891 <KEL>
A.Residues: 1-891 <KEL>
C.Genetice: Embr:U97005; PIDN:AAB52288:1; GSPDB:GN00023; CESP:F19F10.10
C.Genetice:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 TLOPKLIRFIQDK-EYERVG-DPVTRRADVRILAATNRDLGAMVAQGQFREDLLYRLNVI 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 QADLMNLRMELQSYRGSATPAAAKLLTP-AAPRPHNSSRGHRNRRAFPGPEETEQDVDLS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :| || : | | : | 312 VLNLPPLRERAEDILGLAERFLARFYKDYGRPARGFSEAAREAMRQYPWPGNVRE---- 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----YHEEAEOMDELEV 661
                                                                                                                                                                                                                                                                                                                                                                                                                                     7 TLPPPCLCPCSEKGEDMKVGYDPIT-----PQKEEGAVLLSSSFTAMSLYQLAAL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 PCLCFCSEK-----GEDMKVGYDPITPQKEEGAVLLSSSFTAMSLYQLAALQADLMNL
                                                                                                                                                                                                                                                                                                                                                                           26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24; Gaps
                                                                                                                                                                                                                                                                                                              DB 1; Length 449;
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                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                           63;
                                                                                                                                                                                                                                                                                                           6.7%; Score 81; DB:
25.7%; Pred. No. 14;
tive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            619 PSECVLEEEKPRDIFIGTDTEVKKEPIDPE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 RMELQSYRGSATPAAAKLLTPAAPRPHN 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Gene: CESP:F19F10.10
A,Map position: 5
A;Introns: 9/2; 148/2; 243/2; 274/3; 687/2
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Munc13-1 - rat
C, Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 25.74
Matches 37; Conservative
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9

Gaps

32;

37;

Length 613;

163 110

99

GSPDB:GN00068; SPDB:SPCP31B10.07

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C;Accession: B70726
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Comnor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, S37-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-573 <COL>
A;Cross-references: GB:Z77724; GB:AL123456; NID:g3261620; PIDN:CAB01256.1; PID:g1478225
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary; nucleic acid sequence not shown; translation not shown Molecule type: DNA
                                                                                                                                                                                         Č;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                            probable secD - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A/Gene: secD
C/Superfamily: protein export membrane protein secD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.6%; Score 79.5; Di
22.3%; Pred. No. 26;
tive 23; Mismatches
                 736 SENAMGGIYSVLNKKRGHVFSEE 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46; Conservative
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Best Local Similarity
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A.Mocession: 139256
A.Moclece in the Mocken of the Mocken 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    559 PVVSYRESVSEPSSMTALSKSPNKHNRIFMTAEPMSEELSVAIETGHVNPRDDFKVRARI 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    619 MADEFGWDVTDARKIWCF-GPDTTGANVVVDQTKAVAYLNEIKDSVVAAFAWASKEGPMF 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 PC-LCFCSEKGEDMKVGYDPITPQKEEGAVLLSSSFTAMSLYQLAALQADLMNLRMELQ-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.6%; Score 80; DB 2; Length 842; 20.2%; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----AFPGPEETEQD--VDLSAPPALRNIIQD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---AMG---HVIQRKKVHVFGDE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53; Conservative
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Best Local Similarity
Matches 53; Conserv
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Gaps

57;

80; DB 2;

Length 573; Indels

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alpha-galactoside utilization transcription regulator, AraC family protein [imported] - C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: H96037
R;Pinan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan, Proc. Natl. Acad Sci. U.S.A. 98, 9889-9884, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endon A;Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Experimental source: strain 1021, megaplasmid pSymB
B;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, Hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
C;Genetics:
119
                                                                                           207
                                                                                                                                                                                           150
                                                                                                                                                                                                                                                                                                                                                                             202
                                                                                                                                                                                                                                                         268 IS---GDQIQNATSGMDQ-RGIGYVVDLQFKGPAANIWADYTAAHIGTQTAFTLDSQVVS 323
                                                                                      149 AAPPPAQSGAPASPQPGAQPRPYPQDPA-PSPNPTSPASPPPAPPAPATDPRKDLAER
                                                                                                                                                                                           120 -----LRNIIQDCLQLI------ADSDTP-----TIRKGTYTFVPWL
                                                                                                                                                                                                                                                                                                                                                                             151 LSFKRGNALYSQVLYTDPIFAMGHVIQRK----KVHVFGD----ELSLVTLFRCIQNLEE
    74 ATPAAAKLLTPAAPRPHNSSRGHRNRRAFPGPEETEQDVDLSAPPA
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A, Accession: S78484
A, Molecule type: protein
A, Molecule type: protein
A, Residues: 13-20,43-49,68-73,206-209,214-223,235-248,250-262,410-420,443-454,459-470,4,
A, Note: 560-Lys was also found
C, Function:
A, Description: phosphorylates specifically actin in the EGTA-resistant actin-fragmin comes
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Ribin, X.; Kaul, S.; Rounaley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
Ribin, X.; Kaul, S.; Rounaley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Meffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cyclosporin synthetase - cyclosporin fungus
Cispecies: Tolypocladium inflatum (cyclosporin fungus)
Cjate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 03-Nov-2000
CjAccession: 845487; 841309
R;Weber, G.; Schoergendorfer, K.; Schneider-Scherzer, E.; Leitner, B.
R;Weber, G.; 120-125, 1994
A;Title: The peptide synthetase catalyzing cyclosporine production in Tolypocladium nive
A;Reference.number: 845487; WUID:95094306; PMID:80001164
                                                                                                                                                                                                                                                                                                                                                                                                 334 FILRMLRIPHDAIHNPSPSSPSPSPSSS---SSSTSHPTPASSSTSSTLPSSIPSSSNTSP 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPALRNI----IQDC--LQLIADSDTFTIRKGTYTFVPWLLSFKRGNALYSQVLYTDPIF 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----YHSGVLYEGKLY 433
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   A, Cross-references: EMBL: U64722; NID: 91553132; PIDN: AAB08728.1; PID: 91553133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable ATP-dependent RNA helicase A [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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                                                                                                                                                                                                                                       Length 737;
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                                                                                                                                                                                                                                                                                                                                                         26 GYDPITPQKEEGAVLLSSSFTA----MSLYQLAALQADLMNLRMELQ-
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391 PPASSESLVGVEECAWLKVVVPNEKPAPRR-----
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                                                                                                                                                                                                                                       DB 2;
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6.5%; Score 78.5; D
Best Local Similarity 21.1%; Pred: No. 44;
Matches 39; Conservative 31; Mismatches
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29.5%; Pred. No. 66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : : | | :: |
290 L---EPFFASFEVHILHR 304
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Best Local Similarity
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A,Status: preliminary
A,Molecule type: DNA
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A, Map position: 2
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R.Rea, T.J.; Timmins, J.G.; Long, G.W.; Post, L.E.

W. Virol. 54, 21-29, 1986

A. Title: Mapping and sequence of the gene for the pseudorables virus glycoprotein which A; Reference number: A21879; MUD:85135070; PMLD:2983115

A.Accession: A21879

A.Accession: A21879

A.Residues: 1-498 <REA>

A.Residues: 1-498 <REA>

A.Residues: 1-498 <REA>

C. Superfamily: pseudorables virus glycoprotein gX

C. Superfamily: pseudorables virus glycoprotein

C. Superfamily: DNA

C. Superfamily: pseudorables virus glycoprotein

F. S6, 86, 142, 226, 443/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                          RAFPGPEETEQDVDLSAPPALRNIIQDCLQLIADSDTPTIRKGTYTFVPWLLSFKRGNAL 159
                                                                                                                                                                                                                                                            NLRYENRTHR--VRPGETLILLV----PHNHRYWLEEGGRWEFFWISMNGEEALRIHRAI 122
                                                                                                                                                                                                                                                                                                                                                               123 LAVTGPIITLQ-----PDTVEHLADCSLRLIAGGETP----GSAS----AIAYEAAMAL 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307 AEEDEELTSSDLDNIEIEVV---GSPRPPASS-PPPPPPRPPRGRDHDHGHHRADDR 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 GPEETEQDVDLSAPPALRNIIQDCLQLIADSD---TPTIRKGTYTFVPWLLSFKRGNALY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LQADLMNLRMELQSYRGSATPAAAKLLTPAAPRPHNSSRGH-----RNRRAFP 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363 GPORHHR-----LPPE-----PTFVSPSDIFVTPT---GS----PALLLGFLGSALA 402
                                                                                                                                                                                                           ---SSRGHRNR 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----- 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     secreted glycoprotein gx - suid herpesvirus 1
C,Species: suid herpesvirus 1
C,Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                 51; Gaps
                                                                                         Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 498;
                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                             43;
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                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 YDDVFGSHPVLSEEYRKMQHVID----HILGN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                            160 YSQVLYTDPIFA-----MGHVIQRKKVHVFGD 186
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6.5%; Score 78.5; DB
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Matches 55; Conservative 26; Mismatches
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                                                                                                                                                                                                        62 NLRMELQSYRGSATPAAAKLLTPAAPRPHN--
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A, Status: nucleic acid sequence not shown
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                           A; Genome: plasmid
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                                                                                      Query Match
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Matches
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F;11055-11122/Domain: acyl carrier protein homology <ACUB>
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F;12127-12194/Domain: acetate-CoA ligase homology <ACUP>
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A; Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993
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C; Genetics:
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C; Superfamily: cyclosporin fungus cyclosporin synthetase; acetate-CoA ligase homology;
C; Keywords: carrier protein; phosphopantethaine; phosphoprotein
F; 5522-1008/Domain: acetate-CoA ligase homology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3688 ------LTKVPGV------ERIFFGD---MRSHAINRDFLVARAVHALGDKAT 3725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 RGHRNRRAFPGPEE-----TEQDV-----DLSAPPALRNII------QDCL-QLIADS 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.5%; Score 78.5; DB 2; Length 15281;
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10146-10586/Domain: acetate-CoA ligase homology <ACP7>
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1-5057/Domain: acetate-CoA ligase homology <ACL4>
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3, 2004, 07:45:39

Search completed: February Job time: 17.4356 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 3, 2004, 07:43:37; Search time 9.79556 Seconds (without alignments) 1113.790 Million cell updates/sec Run on:

Title: Perfect score:

US-09-911-777-2 1204 1 MDESAKTLPPPCLCFCSEKG......ENAQISRNGDDTFFGALKLL 232 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ļΈ	Q9y275 homo sapien	mus m	O75888 homo sapien	₂		O14460 schizosacch		Q50634 mycobacteri				_			P50872 azospirillu				mus	_		0		_			N	9	6	_	P36956 homo sapien	
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BPHY DEIRA	DPO1 HELPJ	KCH3 MOUSE	KCH3_RAT	SHK1 HUMAN	TYCC_BREPA	TNF6 MACMU	FABD_BUCBP	MIAA CHLTR	YI87 AQUAE	3MG MOUSE	KMLZ_RABIT
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73.5	73.5	73.5	73.5	73.5	73.5	73	73	73	73	73	73
34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

| T13B MOUSE STANDARD; PRT; 309 AA. | 16-OCT-2001 (Rel. 40, | 28-FEB-2003 (Rel. 41, Last annotation update) | Tumor necrosis factor ligand superfamily member |
 | - | se) | Eukaryota, Metazoa, Chordata, | Mammalia: Entheria: Rodentia: | Mammaila; Euclieila; Rouentla;
 | | | | | | | "BAFF, a novel ligand of the tumor necrosis factor family,
 | B cell growth."; | <u>د</u> | [2] | - | STRAIN=NZB; | MEDLINE=21850530; PubMed=11862414; | Jiang Y., Ohtsuji M., Abe M., Li N., Xiu Y., Wen X.S.,
 | Hirose S.; | "Polymorphism and chromosomal mapping of the mouse gene | activating factor belonging to the tumor necrosis factor | | Tww. | <u>+</u> | ٠
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 | -!- STIBUNIT: | SUBCELLIMAR LOCATION TYPE II MEMBRANE PROTEIN ALSO EXISTS AS | EXTRACELLULAR SOLUBLE FORM. |
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 | | the European Bioinformatics Institute. There are no restrictions on | use by non-profit institutions as increased in no | modified and this statement | entities remitted a license | or send an email to license |
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REDINNES FROM N.A. MEDLINE=99288033; PubMed=10359578; Schmedider P., MacKay F., Steiner V., Hofmann K., Schmedider P., MacKay F., Steiner V., Hofmann K., Valmori D., Romero P., Werner-Favre C., Zubler R. Tschopo J.; | 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FRB-2003 (Rel. 41, Last annotation update) 28-FRB-2003 (Rel. 41, Last annotation update) Tumor necrosis factor ligand superfamily member factor) (RAFF). TURST13B OR BAFF. Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Eutheria; Rodentia; Sciurognathi; Muris II CSI TaxID=10090; CSI TaxID=10090; SEQUENCE FROM N.A. MEDLINE=99288033; PubMed=10359578; Schneider P., MacKay F., Steiner V., Hofmann K., Holler N., Ambrose C., Lawton P., Bixler S., Ach Valmori D., Romero P., Werner-Favre C., Zubler R. TSChopp J.; "RAFP, a novel ligand of the tumor necrosis fact | 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FRB-2003 (Rel. 41, Last sequence update) 28-FRB-2003 (Rel. 41, Last annotation update) Tumor necrosis factor ligand superfamily member factor) (RAFF). TURST13 DR BAFF. Mus musculus (Mouse). Rukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Eutheria; Rodentia; Sciurognathi; Muri NCBI TaxID-10090; SEQUENCE FROM N.A. MEDLINE=92288033; PubMed=10359578; Schneider P., MacKay F., Steiner V., Hofmann K., Holler N., Ambrose C., Lawton P., Bixler S., Ach Valmori D., Romero P., Werner-Favre C., Zubler R Tschopp J.; "BAFF, a novel ligand of the tumor necrosis fact B cell growth."; | 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FBB-2003 (Rel. 41, Last sequence update) 28-FBB-2003 (Rel. 41, Last annotation update) Tumor necrosis factor ligand superfamily member factor (BAFF). TNFSF13B OR BAFF. Mus musculus (Mouse). Eukaryota, Metazoa; Chordata; Craniata; Vertebra Mammalia; Eutheria; Rodentia; Sciurognathi; Muri NCBI_TaxID=10090; [1] SEQUENCE FROM N.A. MEDLINE=99288033; PubMed=10359578; Schneider P., MacKay F., Steiner V., Hofmann K., Schneider P., MacKay F., Steiner V., Hofmann K., Schneider P., Romero P., Werner-Favre C., Zubler R. Tschopp J.; "BAFF, a novel ligand of the tumor necrosis fact B cell growth." J. Exp. Med. 189:1747-1756(1999). | 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FRB-2003 (Rel. 41, Last annotation update) 28-FRB-2003 (Rel. 41, Last annotation update) Tumor necrosis factor ligand superfamily member factor) (RAFF). TURST13B OR BAFF. Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Eutheria; Rodentia; Sciurognathi; Muris NCBI_TaxID=10090; [1] SEQUENCE FROM N.A. MEDLINE=99288033; PubMed=10359578; Schneider P., MacKay F., Steiner V., Hofmann K., Holler N., Ambrose C., Lawton P., Bixler S., Ach Valmori D., Romero P., Werner-Favre C., Zubler R. Tschopp J.; TSChopp J.; BAFF, a novel ligand of the tumor necrosis fact B cell growth.; [2] Exp. Med. 189:1747-1756(1999). | 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FRB-2003 (Rel. 41, Last annotation update) Tumor necrosis factor ligand superfamily member factor) (RAFF). TURSTIB OR BAFF. Mus musculus (Mouse). Bukaryota, Metazoa, Chordata, Craniata, Vertebra Mammalia; Butheria, Rodentia, Sciurognathi, Muri NCBI TaxID=10090; SCHIELINE=99288033; PubMed=10359578; SCHIELINE=99288033; PubMed=10359578; SCHIEGER N., Ambrose C., Lawton P., Bixler S., Ach Valmori D., Romero P., Werner-Favre C., Zubler R. Tschopp J.; "BAFF, a novel ligand of the tumor necrosis fact B call growth."; J. Exp. Med. 189:1747-1756(1999). 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[2] SEQUENCE FROM N.A., AND VARIANT SER-79. STRAIN=NZB; MEDLINE=21850530; PubMed=11862414; Jiang Y., Ohtsuji M., Abe M., Li N., Xiu Y., Wen Hirose S.; Polymorphism and chromosomal mapping of the mou activating factor belonging to the tumor necrosi (Baff) and association with the autoimmune phenoimmunogenetics 53:810-813(2001). - FUNCTION: Cytokine that binds to TNFRSF13B/T TRYNSF13/APRIL binds to the same 2 receptors and T-cell function and the regulation of hut hird B-cell specific BAFFF Rel survival of mature B-cells and the B-cell religious L. SUBGELLULAR LOCATION: TYPE II MEMBRANE PROFE | 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FRB-2003 (Rel. 41, Last sequence update) 28-FRB-2003 (Rel. 41, Last sequence update) Tumor necrosis factor ligand superfamily member factor) (BAFF). TURSF13B OR BAFF. Mus musculus (Mouse). 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MEDLINE=9928803; PubMed=10159578; Schndoider P., MacKay F., Steiner V., Hofmann K., Holler N., Ambrose C., Lawton P., Bixler S., Ach Valmori D., Romero P., Werner-Favre C., Zubler R. Tschopp J.; "BAFF, a novel ligand of the tumor necrosis fact B cell growth."; "BAFF, a novel ligand of the tumor necrosis fact B cell growth."; "BAFF, and an ovel ligand of the tumor necrosis fact B cell growth."; J. Exp. Med. 189:1747-1756(1999). [2] Exp. Med. 189:1747-1756(1999). [2] Exp. Med. 189:1747-1756(1999). [2] WEDLINE=21850530; PubMed=11862414; Jiang Y., Ohtsuji M., Abe M., Li N., Xiu Y., Wen Hirose S.; MEDLINE=21850530; PubMed=11862414; Jiang Y., Ohtsuji M., Abe M., Li N., Xiu Y., Wen Hirose S.; "Polymorphism and chromosomal mapping of the mou activating factor belonging to the tumor necrosis (Baff) and association with the autoimmune pheno Immunogenetics 53:810-813(2001)!- FUNCTION: Cytokine that binds to TNFRSF13B/T TNFSF13AP/T TNF | 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) TUMCY necrosis factor ligand superfamily member factor) (BAFF). TURSF13B OR BAFF). Mus musculus (Mouse). Bukaryota, Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Rodentia; Sciurognathi; Murin NCB1_TAXID=10090; [1] SEQUENCE FROM N.A. MEDLINE=92288033; PubMed=10359578; Schneider P., MacKay F., Steiner V., Hofmann K., Schneider P., MacKay F., Steiner V., Hofmann K., Valmori D., Romero P., Werner-Favre C., Zubler R Tschopp J.; Rowero P., Werner-Favre C., Zubler B call growth."; J. Exp. Med. 189:1747-1756(1999). SEQUENCE FROM N.A., AND VARIANT SER-79. STRAIN=NZB; MEDLINE=21850530; PubMed=11862414; Jiang Y., Ohtsuji M., Abe M., Li N., Xiu Y., Wen Hiroge S.; Jiands Y., Ohtsuji M., Abe M., Li N., Xiu Y., Wen Hiroge S.; Jiang Y., Ohtsuji M., Abe M., Li N., Xiu Y., Wen Hiroge S.; Jiang Y., Ohtsuji M., Abe M., Li N., Xiu Y., Wen Hiroge S.; Jiang Y., Chill binds to the same 2 receptors 1 Immunogenetics 33:810-813(2001). 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189:1747-1756(1999). SEQUENCE FROM N.A., AND VARIANT SER-79. STRAIN=NZB; MEDLINE=21850530; PubMed=11862414; Jiang Y., Ohtsuji M., Abe M., Li N., Xiu Y., Wen Hirose S.; MPOLymorphism and chromosomal mapping of the mou activating factor belonging to the tumor necrosi (Baff) and association with the autoimmune pheno Immunogenetics 53:810-813(2001). | 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Tumor necrosis factor ligand superfamily member factor) (BAFF). Mus musculus (Mouse). Bukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Rodentia; Sciurognathi; Muris NCBI_TaxID=10090; [1] MEDLINE=99288033; PubMed=10159578; Scholler ROM N.A. MEDLINE=99288033; PubMed=10159578; Scholler N., Ambrose C., Lawton P., Bixler S., Ach Valmori D., Romero P., Werner-Favre C., Zubler R. Tschopp J.; "BAFF, a novel ligand of the tumor necrosis fact B cell growth."; J. Exp. Med. 189:1747-1756(1999). [2] SEQUENCE FROM N.A., AND VARIANT SER-79. STRAIN-BAZB; MEDLINE=21850530; PubMed=11862414; Jiang Y., Ohtsuji M., Abe M., Li N., Xiu Y., Wen Hirose S.; "Polymorphism and chromosomal mapping of the mou activating factor belonging to the tumor necrosi (Baff) and association with the autoimmune pheno Immunogenetics 53:810-813(2001). | 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Tumor necrosis factor ligand superfamily member factor) (BAFF). Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Eutheria; Rodentia; Sciurognathi; Muri NCBI_TaxID=10090; [1] SEQUENCE RROM N.A. MEDLINE=992880313 PubMed=10359578; Schmeider P., Mackey F., Steiner V., Hofmann K., Holler N., Ambrose C., Lawton P., Bixler S., Ach Valmori D., Romero P., Werner-Favre C., Zubler R. Tschopp J.; "BAFF, a novel ligand of the tumor necrosis fact B cell growth."; J. Exp. Med. 189:1747-1756(1999). [2] STRAIN=NZB, MEDLINE=21850530; PubMed=11862414; Jiang Y., Ohtsuji M., Abe M., Li N., Xiu Y., Wen Hirose S., Ohtsuji M., Abe M., Li N., Xiu Y., Wen Hirose S., "Potsujism and chromosomal mapping of the mou activating factor belonging to the tumor necrosi (Baff) and association with the autoimmune phenoimmunogenetics 53:810-813(2001). -I FUNCTION: Cytokine that binds to TNFRSF13B/T TNFSF13APRIL binds to the same 2 receptors and T-cell function and the regulation of huthird B-cell specific BAFF-receptor (BAFFR/F) survival of mature B-cells and the B-cell resurvival PHM: THE SOLUBLE FORM DERIVES FROM THE MEMBER | 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Tumor necrosis factor ligand superfamily member factor) (BAFF). Mus musculus (Mouse) Bukaryota, Metazoa; Chordata; Craniata; Vertebra Mammalia; Eutheria; Rodentia; Sciurognathi; Murin NCBI_TaxID=10090; [1] SEQUENCE FROM N.A. MEDLINE=99288033; PubMed=10359578; Schneider P., MacKay F., Steiner V., Hofmann K., Schneider P., MacKay F., Steiner V., Hofmann K., Valmori D., Romero P., Werner-Favre C., Zubler R Tschopp J.; Schopp J.; Schorider P., MacKay F., Steiner V., Hofmann K., Valmori D., Romero P., Werner-Favre C., Zubler R Tschopp J.; Schorider P., MacKay F., Steiner V., Hofmann K., Valmori D., Romero P., Werner-Favre C., Zubler R Tschopp J.; Schorider P., Mousuli M.A., AND VARIANT SER-79. STRAIN=NZB, MCDIINE=21850530; PubMed=11862414; Jiang Y., Ohtsuji M., Abe M., Li N., Xiu Y., Wen Hirose S.; "Polymorphism and chromosomal mapping of the mou activating factor belonging to the tumor necrosi (Baff) and association with the autoimmune pheno Immunogenetics 53:810-813(2001) | 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Tumor necrosis factor ligand superfamily member factor) (BAFF). Mus musculus (Mouse) Bukaryota; Metazoa; Chordata; Craniata; Vertebra Musmmalia; Eutheria; Rodentia; Sciurognathi; Muri NCBI_TaxID=10090; [1] SEQUENCE FROM N.A. MEDLINE=99288033; PubMed=10159578; SCHOMICE PO, MacKay F., Steiner V., Hofmann K., Ach Valmori D., Romero P., Werner-Pavre C., Zubler R. Tschopp J.; RAPF, a novel ligand of the tumor necrosis fact B cell growth."; J. Exp. Med. 189:1747-1756(1999). [2] Exp. Med. 189:1747-1756(1999). [2] SEQUENCE FROM N.A., AND VARIANT SER-79. STRAIN-BUZB; MEDLINE=21850530; PubMed=11862414; Jiang Y., Ohtsuji M., Abe M., Li N., Xiu Y., Wen Hirose S.; "Polymorphism and chromosomal mapping of the mou activating factor belonging to the tumor necrosi (Baff) and association with the autoimmune phenoimmunogenetics 53:810-813(2001). I-FUNCTION: Cytokine that binds to TMFRSFI38/T TMSFI3/APRIL binds to the same 2 receptors and T-cell function and the regulation of huthir Association and the regulation of huthir and T-cell function and the regulation of the third B-cell specific BAFF-receptor (BAFFR/FR) survival of mature B-cells and the B-cell resulting Recorder SISSUNG SUBGNIT: Homotrimer SU
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MEDLINE=92288033; PubMed=10359578; Schneider P., MacKay F., Steiner V., Hofmann K., Holler N., Ambrose C., Lawton P., Bixler S., Ach Valmori D., Romero P., Werner-Favre C., Zubler R TSchopp J.; Ambrose C., Lawton P., Bixler S., Ach Valmori D., Romero P., Werner-Favre C., Zubler R TSchopp J.; Ohtsuji M., Abb M., Li N., Xiu Y., Wen Hirose S.; STRAIN-NZB; MEDLINE=21850530; PubMed=11862414; Jiang Y., Ohtsuji M., Abe M., Li N., Xiu Y., Wen Hirose S.; TONCTION: Cytokine that binds to TNFRSF13B/T TNFSF13/APRIL binds to the same 2 receptors 2 ligands -2 receptors pathway involved in tand T-cell function and the regulation of buthird B-cell specific BAFF-receptor (BAFFR/B SUTVIVIA B-CEll function and the regulation of buthird B-cell specific BAFF-receptor (BAFFR/B SUTSTAIN-ROLELULAR SOLUBLE FORM DERIVES FROM THE MEMBER PROTEOLYTIC PROCESSING. | | · · · · · · | 16-077-2001 (Rel. 40, List sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Tumor necrosis factor ligand superfamily member 13B (B cell-activating factor) (BAFP: Wis musculus (Mouse) Education (Mouse) Rukaryota, Metazoa) Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria, Rodentia; Sciurognathi; Muridae; Murinae; Muss. NUSI TaxID=10090; (I) TaxID=10090; (I) TaxID=10090; (I) Romero P., Wackay P., Steiner V., Hofmann K., Bodmer JL., Hollor N., Ambrose C., Lawton P., Bixler S., Acha-Corboa H., Hollor N., Ambrose C., Lawton P., Bixler S., Acha-Corboa H., Tachopp J.; Romero P., Werner-Favre C., Zubler R.H., Browning J.L., Tachopp J.; Romero P., Werner-Favre C., Zubler R.H., Browning J.L., Tachopp J.; Romero P., Warner-Favre C., Zubler R.H., Browning J.L., Tachopp J.; Romero P., Warner-Favre C., Zubler R.H., Browning J.L., Tachopp J.; Romero P., Warner-Favre C., Zubler R.H., Browning J.L., Tachopp J.; Romero P., Warner-Favre C., Zubler R.H., Browning J.L., Tachopp J.; Romero P., Warner-Favre C., Zubler R.H., Browning J.L., Tachopp J.; Romero P., Warner-Favre C., Zubler R.H., Browning J.L., Tachopp J.; Romero P., Warner-Favre C., Zubler R.H., Browning J.L., Tachopp J.; Romero P., Warner-Favre C., Zubler R.H., Browning J.L., Tachopp J.; Romero P., Warner-Favre C., Zubler R.H., Browning J.L., Tachopp J.; Romero P., Mannari Sarail T., Hirose S.; Polymorphism and chromosomal mapping of the mouse gene for B-cell activating factor belonging to the tumor necrosis factor family Targes S.; Romero P., Parray Involved in the stimulation of the survival of mature B-cell specific BarF-receptor (BaFF/RS) promotes the survival of mature B-cells and the B-cell response | 16-077-2001 (Rel. 40, List sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Tumor necrosis factor ligand superfamily member 13B (B cell-activating factor) (BAFP). TWFSF13B OR BAFP. Wis macculus (Mouse). Eukaryotes, Metazoa; Chiordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090; [1] SEQUENCE FROM N.A. MEDLINE=9288033; PubMed=1035957B; Schneider P., MacKay F., Steiner V., Hofmann K., Bodmer JL., Holler N., Ambrose C., Lawron P., Bixler S., Ana-Orboa H., Valmori D., Romero P., Wenner-Favre C., Zubler R.H., Browning J.L., Holler N., Ambrose C., Lawron P., Bixler S., Ana-Orboa H., Valmori D., Romero P., Wenner-Favre C., Zubler R.H., Browning J.L., Holler N., Ambrose C., Lawron P., Bixler S., Ana-Orboa H., Stapin S., Ana-Orboa H., Valmori D., Romero P., Wenner-Favre C., Zubler R.H., Browning J.L., Holler N., Ambrose C., Lawron P., Bixler S., Ana-Orboa H., Stapin S., Ana-Orboa H., Li N., Xiu Y., Wen X.S., Shirrai T., Hirose S., Shirai T., Hirose S., Shirai T., Hirose S., Shirai M., Abe M., Li N., Xiu Y., Wen X.S., Shirrai T., Hirose S., Jangorphi H., And P. 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MECKAY F., Steiner V., Hofmann K., Bodmer JL., Holler N., Ambrose C., Lawton P., Bixler S., Acha-Orbea H., Valmori D., Romero P., Werner-Favre C., Zubler R.H., Browning J.L., Holler N., Ambrose C., Lawton P., Bixler S., Acha-Orbea H., Valmori D., Romero P., Werner-Favre C., Zubler R.H., Browning J.L., Holler N., Ambrose C., Lawton P., Bixler S., Acha-Orbea H., Valmori D., Romero P., Werner-Favre C., Zubler R.H., Browning J.L., Holler N., Ambrose C., Lawton D., Bixler S., Acha-Orbea H., Medil J., And Lassing C., Lawton D., Browning J.L., Medil J., And Lassing C., Lawton D., Browning J.L., Medil J. Scoul B., Marker L. M., Xiu Y., Wen X.S., Shirai T., Medil J. Scoul L. Scoul Lassing C. Lawton D., Medil J. A., And Warlay T.SER-79. SEQUENCE FROM N.A., Abb W., Li N., Xiu Y., Wen X.S., Shirai T., Medil J., And J., And Warlay Engling to the tumor necrosis factor family J. And association with the autoimmune phenotype."; Immunogenetics 53:810-813(2001). Immunogenetics 53:810-813(2001). 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Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch). | Valmori D., Romero P., Werner-Pavre C., Zubier R.H., Browning J.L., TabkPr, a novel ligand of the tumor necrosis factor family, stimulates B cell growth."; J. Exp. Med. 189:1747-1756(1999). [2] SEQUENCE FROM N.A., AND VARIANT SER-79. STRAINBAIRS MEDLINS-21850530; PubMed=11862414; Jiang Y., Ohtsujj M., Abe M., Li N., Xiu Y., Wen X.S., Shirai T., "Plymorphism and chromosomal mapping of the mouse gene for B-cell activating factor belonging to the tumor necrosis factor family activating factor belonging to the tumor necrosis factor family immunogenetics 53:810-813(2001). | "BARP, a novel ligand of the tumor necrosis factor family, stimulates B call growth."; J. Exp. Med. 189:1747-1756(1999). [2] SEQUENCE FROM N.A., AND VARIANT SER-79. 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STRAIN=NZB; MEDLINE=21850530; PubMed=11862414; Jiang Y., Ohtsuji M., Abe M., Li N., Xiu Y., Wen X.S., Shirai T., Hirose S.; "Polymorphism and chromosomal mapping of the mouse gene for B-cell activating factor belonging to the tumor necrosis factor family (Baff) and association with the autoimmune phenotype."; Immunogenetics 53:810-813(2001) -!- FUNCTION: Cytokine that binds to TNFRSF13B/TACI and TNFRSF17/BCMA. TNFSF13/APRIL binds to the same 2 receptors. Together, they form a 2 ligands -2 receptors pathway involved in the stimulation of B- and T-cell function and the regulation of humoral immunity. A third B-cell specific BAFF-receptor (BAFFR/BR3) promotes the survival of mature B-cells and the B-cell response!- SUBCELLULAR SOLUBLE FORM!- SUBCELLULAR SOLUBLE FORM!- FUNCTION: TYPE II MEMBRANE FORM BY PROTECLIVIAR SOLUBLE FORM!- STRACELLULAR SOLUBLE FORM!- SIMILARITY: Belongs to the tumor necrosis factor family. This SWISS-RROT entry is copyright. 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STRAIN=1286 MEDLINE=1286530; PubMed=11865414; Jiang Y., Ohtsuji M., Abe M., Li N., Xiu Y., Wen X.S., Shirai T., Jiang Y., Ohtsuji M., Abe M., Li N., Xiu Y., Wen X.S., Shirai T., "Polymorphism and chromosomal mapping of the mouse gene for B-cell activating factor belonging to the tumor necrosis factor family [BAEf] and association with the autoimmune phenotype."; Imminogenetics 53:810-813(201) | MEDLINE=21850530; PubMed=11862414; Jiang Y., Ohtsuji M., Abe M., Li N., Xiu Y., Wen X.S., Shirai T., Hirose S.; Hirose S. | MEDLINE=21850530; PubMed=11862414; Jiang Y., Ohtsuji M., Abe M., Li N., Xiu Y., Wen X.S., Shirai T., Hirose S.; "Polymorphism and chromosomal mapping of the mouse gene for B-cell activating factor belonging to the tumor necrosis factor family (BAET) and association with the autoimmune phenotype."; Immunogenetics 53:810-813(2001)!- FUNCTION: Cytokine that binds to TNFRSF13H7ACI and TNFRSF17/BCMA!- FUNCTION: Cytokine that binds to TNFRSF13H7ACI and TNFRSF17/BCMA!- FUNCTION: Cytokine that binds to TNFRSF13H7ACI and TNFRSF17/BCMA!- FUNCTION: Cytokine that binds to the same 2 receptors Together they form a 2 ligands -2 receptors pathway involved in the stimulation of B- and T-cell function and the regulation of humoral immunity. 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FTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTECLULAR SOLUBLE FORM. -! SIMILARITY: Belongs to the tumor necrosis factor family. This SWISS-PROT entry 1s copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstatic the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (see http://www.isb-sib.ch/announor send an email to license@isb-sib.ch). | Hirose S.; "Polymorphism and chromosomal mapping of the mouse gene for B-cell activating factor belonging to the tumor necrosis factor family (Baff) and association with the autoimmune phenotype."; Immunogenetics 5:810-813(2001)! FUNCTION: Cytokine that binds to TNFRSF13B/TACI and TNFRSF17/BCMA. TNFSF13/APRIL binds to the same 2 receptors. 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Usage by and for commercentifies requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch). | "Polymorphism and chromosomal mapping of the mouse gene for B-cell activating factor belonging to the tumor necrosis factor family (Baff) and association with the autoimmune phenotype."; Imminogenetics 53:810-813(2001). -i- FUNCTION: Cytokine that binds to TNFRSF13B/TACI and TNFRSF17/BCMA. TNFSF13/APRIL binds to the same 2 receptors. Together, they form a 2 ligands -2 receptors pathway involved in the stimulation of B- and T-cell function and the regulation of humoral immunity. A third B-cell specific BAFF-receptor (BAFFR/BR3) promotes the survival of mature B-cells and the B-cell response. -i- SUBGELLULAR BOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM. -i- FUNCELLULAR SOLUBLE FORM. -i- FUNCEDIAL FORM DERIVES FROM THE MEMBRANE FORM BY PROTEOLYTIC PROCESSING. -i- SIMILARITY: Belongs to the tumor necrosis factor family. This SWISS-ROT entry is copyright. It is produced through a collaborat the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in in mo modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/announor send an email to license@isb-ch). | activating factor belonging to the tumor necrosis factor family (Baff) and association with the autoimmune phenotype."; Immunogenetics 5:310-813(001). -!- FUNCTION: Cytokine that binds to TNFRSF13/ARCI and TNFRSF17/BCMA. -!- FUNCTION: Cytokine that binds to TNFRSF13/ARCI and TNFRSF17/BCMA. 2 ligands -2 receptors pathway involved in the stimulation of B- and T-cell function and the regulation of humoral immunity. A third B-cell specific BAFF-receptor (BAFFNRB3) promotes the survival of mature B-cells and the B-cell response. -!- SUBUNIT: Homotrimer. -!- SUBUNIT: Homotrimer. -!- FTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTELLULAR SOLUBLE FORM. -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTELLULAR SOLUBLE FORM. -!- SIMILARITY: Belongs to the tumor necrosis factor family. This SWISS-PROT entry is copyright. 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 | -!- SUBUNIT: Homotriner!- SUBUNIT: Homotriner!- SUBUNIT: Homotriner!- SUBULIT: HOMOTRINER LOCATION: TYPE II MEWBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTECLYTIC PROCESSING!- SIMILARITY: Belongs to the tumor necrosis factor family!- SIMILARITY: Belongs to copyright. It is produced through a collaborat between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commerce entities requires a license@isb-sib.ch). | -i- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM. -i- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTECLYTIC PROCESSING. -i- SIMILARITY: Belongs to the tumor necrosis factor family. This SWISS-PROT entry is copyright. It is produced through a collaborat between the Swiss Institute of Bioinformatics and the EMBL outstatic the European Bioinformatics Institutions as long as its content is in no modified and this statement is not removed. Usage by and for commerce entities requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch). | EXTRACELLULAR SOLUBLE FORM. -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTEOLYTIC PROCESSING1- SIMILARITY: Belongs to the tumor necrosis factor family. This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstatic the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch).
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MEMBER 13B, SOLUBLE FORM.
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(FOTENTIAL).
EXTRACELLULAR (POTENTIAL).
CLEAVAGE (BY SIMILARITY).
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Shu H.-B., Hu W.-H., Johnson H.;
"TALL-1 is a novel member of the TNF family that is down-regulated by
                                                                          TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
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16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor ligand superfamily member 13B (TNF-and APOL-related leukocyte expressed ligand 1) (TALL-1) (B lymphocyte stimulator) (BLyS) (B cell-activating factor) (BAFF) (Dendritic cell-derived TNF-like molecule)
TNFSF13B OR TALL1 OR BLYS OR BAFF OR ZTNF4.
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TISSUE=Placenta;

X Studence, Feingold E.A., Gruse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Gruse L.H., Derge J.G.,

A Rlausner R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haiteh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nollalon D.K., Muxny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Notiguez A.C., Grimwood J., Schmutz J., Myers R.M.,

B Schnertield Y.S.N., Krzywinski M.I., Skalska W., Sanilus D.E.,

B Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                             "BAFF, a novel ligand of the tumor necrosis factor family, stimulates B cell growth.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M. McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Quo J., Stolina M., Boyle W.J., Sarosi I., Hau H., Senaldi G., Theill L.B., "APRIL and TALL I and receptors BCMA and TACI: system for regulating
                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 134-148.
MEDLINE=99288033; PubMed=10359578;
Schneider P., MacKay F., Steiner V., Hofmann K., Bodmer J.-L.,
Holler N., Ambrose C., Lawton P., Bixler S., Acha-Orbea H.,
Valmori D., Romero P., Werner-Favre C., Zubler R.H., Browning J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUB=Monocytes, and Neutrophils;
MEDLINE=99329343; PubMed=10398604;
Moore P.A. Belvedere O., Orr A., Pieri K., LaFleur D.W., Feng P., Soppet D., Charters M., Gentz R., Parmelee D., Li Y., Galperina O., Grept J., Roschke V., Nardelli B., Carrell J., Sosnovtseva S., Greenfield W., Ruben S.M., Olsen H.S., Fikes J., Hilbert D.M.;
"BLyS: member of the tumor necrosis factor family and B lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-135 FROM N.A., AND VARIANT THR-105.
Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;
"New polymorphisms of human BLyS gene.",
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang W., Wan T., Yu Y., Cao X.;
"A novel dendritic cell-derived TNF-like molecule.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Farrah T., Gross J., Piddington C., O'Hara P.; "Home sapiens homelog of tumor necrosis factor."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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mitogens.";
J. Leukoc. Biol. 65:680-683(1999).
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[9]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                 **RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 134-285.

**REDLIBE=1912420; PubMed=11862220;
Oren D.A., Li Y., Volovik Y., Morris T.S., Dharia C., Das K.,
Galperina O., Genter R., Arnold E.,
"Structural basis of BLyS receptor recognition.";
"Struct. Biol. 9:288-29(2002).

'I. FUNCTION: Cytokine that binds to TNPRSF13B/TACI and TNPRSF17/BCMA.

'I. FUNCTION: Cytokine that binds to TNPRSF13B/TACI and TNPRSF17/BCMA.

ITRPSF13/APRIL binds to the same 2 receptors. Together, they form a 2 ligands - 2 receptors pathway involved in the stimulation of B-
and T-cell function and the regulation of humoral immunity. A third B-cell specific BAFF-receptor (BAFFR/BR3) promotes the
                                                                                                                                                                                                                                                                                                                                                                                                                                            survival of mature B-cells and the B-cell response.
SUBDAT: HOMOSTINE.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN PERIPHERAL BLOOD LEUROCYTES AND IS SPECIFICALLY EXPRESSED IN MONCYTES AND MACROPHAGES, ALSO FOUND IN THE SPLEEN, LYMPH NODE, BONE MARROW CELLS AND DENDRITIC CELLS. A LOWER EXPRESSION SEEN IN PLACENTA,
                                                                                                                                  MEDLINE=21686304; PubMed=11827482; Karpusas M., Cachero T.G., Qian F., Boriack-Sjodin A., Mullen C., Strauch K., Hsu Y.-M., Kalled S.L.; Crystal structure B. Stracellular human BAFF, a TNF family member that stimulates B lymphocytes."; J. Mol. Biol. 315:1145-1154(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytokine, Transmembrane, Glycoprotein; Signal-anchor; 3D-structure;
Polymorphism.
                               Liu Y., Xu L., Opalka N., Kappler J., Shu H.-B., Zhang G.; "Crystal structure of sTALL-1 reveals a virus-like assembly of TNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEART, LUNG, FETAL LIVER, THYMUS, AND PANCREAS.
INDUCTION: UPREGULATED BY EXPOSURE TO INTERFERON-GAMMA. DOWN-REGULATED BY PHORBOL MYRISTATE ACETATE/IONOMYCIN TREATMENT.
PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
PROTEOLYTIC PROCESSING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell proliferation; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to the tumor necrosis factor family.
X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 142-285.
                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 136-285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0008283; P:cell proliferation; TAS. GO; GO:0008284; P:positive regulation of ce GO; GO:000165; P:signal transduction; TAS. InterPro; IPR006052; TNF family.
SWART; SWO207; TNF 1.
PROSITE; PS00251; TNF 1.
PROSITE; PS0049; TNF 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO:0005625; C:soluble fraction; TAS
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                                                                   family ligands.";
Cell 108:383-394(2002).
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60 CLTVVSFYQVAALQGDLASLRABLQGHHABKLPAGAGAPKAGLBEAPAVTAGLKIFEPPA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 PRPHNSSRGHRNRRAFPGPEETEQDVDLSAPPALRNIIQDCLQLIADSDTPTIRKGTYTF
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            TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 13B, SOLUBLE FORM.
CYTOPLASMIC (POTENTIAL).
                                                                 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Q9D777; Q9ERP1;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member 13 (A proliferation-inducing ligand) (APRIL).
                                                                                                                                                         (GLCNAC. . .). (HIGH MANNOSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEMBER 13B, MEMBRANE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31222 MW; 48ED0D7AB38C8867 CRC64;
                                                                                     (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.7%; Score 622.5; DB 1;
48.7%; Pred. No. 3.3e-51;
ive 23; Mismatches 48;
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N-LINKED
                                                                                                                      CLEAVAGE
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48.78; Fr.
23; P
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Best Local Similarity 48.7<sup>3</sup>
Matches 146; Conservative
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DISULFID
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CARBOHYD
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RESULT 4
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RA MEDINE=21085660; PubMed=1121851;

RA Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aito T., Satao M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Asato T., Okazaki Y., Gojobori T., Bono H., Raulov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

R. Fleischmann W., Gassterland T., Gissi C., Kinig B., Kochiwa H.,

R. Kuchl P., Lewis S., Matsuvo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Bult C., Fleicher C., Fujita M., Gariboldi M.,

RA Brownstein M.J., Bult C., Fleicher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Saski H., Sato K., Schoenbach C., Seya T., Sakamoto N.,

RA Saski H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Hayashizaki Y., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Hayashizaki Y., Toxo-oka K., Wang K.H., Kawaji H., Kohtsuki S.,

R. "Functional annottaion of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                 Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M., McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M., Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E., "APRIL and TALL-I and receptors BCMA and TACI: system for regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:008284; P:positive regulation of cell.proliferation; IDA.
InterPro; IRR006052; TNF_family.
Pfam; PF00229; TNF; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS000251; TNF_1; 1.
PROSITE; PS000251; TNF_2; 1.
Cytokine; Immune response; Glycoprotein.
PROPEP

CHAIN 96 241 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 13.
SITE 95 05 CLEANAGE (BY FURIN) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
N-LINKED (GLCNAC. . .) (POTENTIAL)
MISSING (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001).

-!- FUNCTION: Cytokine that binds to TNFRSF13B/TACI and to TNFRSF17/BCMA. May be implicated in the regulation of tu growth. May be involved in monocyte/macrophage-mediated immunological processes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteolytic processing.
--- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Secreted (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4B96D03BDBC712A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: Homotrimer (Potential).
                                                               TISSUE=Lung;
MEDLINE=21170294; PubMed=10973284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF294825; AAG22534.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AK009514; BAB26332.1; -.
                                                                                                                                                                                                   Nat. Immunol: 1:252-256(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26889 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGI:1916833; Tnf8f13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96
202
115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95
187
115
120
241 AA;
                                                                                                                                                                               humoral immunity.";
                                             FROM N.A
       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
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12.5%; Score 151; DB 1; Length 241;

Query Match

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9
                                                                                                                                          93 -----SRGHRNRRAFPGPEETEQDVDLSAPPALRNIIQDCLQLIADSDTPTIRKG 142
                                                                                                                                                                                                                         ----LYSQVLYTDPIFAMGHVIQRKKVHVFG 185
                                                                                                                                                                                                                                             92
                                                                                                   77
                                                                                       27 GAVLGAVTCAVALLIQ----QTELQSLRREVSRLQRSGGPSQKQ-----GERPWQSLWEQ
                                                                                                                                                                                                                                                                                                      186 DELSLYTLFRCIQ--------NLEEGDEIQLAIPRENAQISRNGDDTFF
                                                                 37 GAVLLSSSFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAAKLLTPAAPRPHNS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99260341; PubMed=10331498;
Shu H.-B., Hu W.-H., Johnson H.;
"TALL-1 is a novel member of the TNF family that is down-regulated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUB-Uterus;
MEDLINE-98416181; PubMed-9743536;
MEDLINE-98416181; PubMed-9743536;
Hahne M., Kataoka T., Schroeter M., Hofmann K., Irmler M.,
Bodmer J.-L., Schneider P., Bornand T., Holler N., French L.E.,
Sordat B., Rimoldi D., Tschopp J.;
"APRIL, a new ligand of the tumor necrosis factor family, stimulates
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TW13 HUMAN STANDARD; PRT; 250 AA.

075888; Q96HV6; Q9PIM8; Q9PIM9;
16-0CT-2001 (Rel. 40, Created)
15-SEP-2003 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-Muor necrosis factor ligand superfamily member 13 (A proliferation-inducing ligand) (APRIL) (TNF-and APOL-related leukocyte expressed ligand 2) (TALL-2) (TNF-related death ligand-1) (TRDL-1).

TNFSF13 OR APRIL OR TALL2 OR ZTNF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Farrah T., Grant F., Haldeman B., Whitmore T., Gross J., O'Hara P., "Homo sapiens tumor necrosis factor homolog.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA AND GAMMA).
MEDLINE-20168636; PubMed=10706119;
KRELLY KA., Manos E.J., Jones D.T., Nadauld L., Jones D.A.;
"APRIL/TRDL-1, a tumor necrosis factor-like ligand, stimulates cell
                                                                                                                                                                                  78 SPDVLEAWKDGAKSRRRRAVLTQKHKKKHSVLHLVPV--NITSK-----ADSDV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                            80,
                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
        6.1e-07;
thes 75;
        26.9%; Pred. No. 6.1e-
:ive 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitogens.";
J. Leukoc. Biol. 65:680-683(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUB=Ovary;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Exp. Med. 188:1185-1190(1998).
                                                                                                                                                                                                                         143 TYTFVPWLLSFKRGNA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cancer Res. 60:1021-1027(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-247 FROM N.A.
                          66, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                growth.".
Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  227 GALKL 231
                                                                                                                                                                                                                                                                                                                                                                                                          1 : | |
237 GFVKL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumor cell
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HGNC:11928; TNFSF13.

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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Marusina K., Sarahina G.M., Hong L., A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hallyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., A Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman M.W. Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schmerch A., Schein I.S., Jones S.J.M., Marra M.A., Generation and initial analysis of more than 15,000 full-length Marra Marl Mouse CDNA sequences M. Marra M.A., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M., McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Gub J., Stolina M., Bbyle W.J., Sarosi I., Hau H., Senaldi G., Theill L.E., "APRIL and TALL-I and receptors BCMA and TACI: system for regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN TRANSFORMED CELL LINES, CANCERS OF COLON, THYROID, LYMPHOID TISSUES AND SPECIFICALLY EXPRESSED IN MONOCYTES AND MACROPHAGES.
INDUCTION: DOWN-REGULATED BY PHORBOL MYRISTATE ACETATE/IONOMYCIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumor cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROCESSING BY FURIN, MUTAGENESIS OF ARG-101 AND ARG-104, AND SUBCELLULAR LOCATION.

MEDLINE=21486098; PubMed=11571266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- PTM: The precursor is cleaved by furin.
-1- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=075888-2; Sequence=VSP_006450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=075888-3; Sequence=VSP_006451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Alpha;
Isold=075888-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunological processes.
-!- SUBUNIT: Homotrimer (Potential).
-!- SUBCELLULAR LOCATION: Secreted.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21170294; PubMed=10973284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          humoral immunity.";
Nat. Immunol. 1:252-256(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF046888; AAC61312.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF136294; AAD29422.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Gamma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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AF114013; AAF59830.1; BC008042; AAH08042.1;

AF184972; AAF01321.1 AF114012; AAF59829.1

AF114011;

EMBL; EMBL; EMBL; EMBL;

EMBL;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---RGHRNRRAFP 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :: : | | : : | | 1.3 | 1.08 TQKQKKQHSVLHLVP-INATSKD------DSDV-----TEVMMQPALRRGRGLQAQG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 LLTQQTELQSLRREVSRLQGTGGPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRAVL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 YGVRIQDAGVYLLÝSQVLFQDVTFTMGQVVSRE-----GQGRQETLFRCIRSMPSHPDR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jang W., Weber J.S., Bashir R., Bushby K., Meisler M.H.,
"Aupl, a novel gene on mouse chromosome 6 and human chromosome 2pl3.",
Genomics 36:366(368(1996).
-!- TISSUE SPECIFICITY: Ubiquitous.
-!- SIMILARITY: BELONGS TO THE AUPI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 GPEETEQDVDLSAPPALRNIIQDCLQLIADSDTPTIRKGTYTFVPWLLSFKRGNA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. ..) (POTENTIAL).
KQHSVLHLVPINATSKD -> N (in isoform Beta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         usa muscuria (moduse).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----LYSQVLYTDPIFAMGHVIQRKKVHVFGDELSLVTLFRCIQ----
                                                                            cell proliferation; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTIG=VSP_006451.
RKRR->AKRA: ABOLISHES PROTEOLYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 149; DB 1; Length 250; Pred. No. 9.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 AYNSCYSAGVFHLHQGDILSVIIPRARAKLNLSPHGTFLGFVKL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------NLEEGDEIQLAIPRENAQISRNGDDTFFGALKL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=VSP_006450.
Missing (in isoform Gamma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N -> S (IN REF. 5).
F -> L (IN REF. 5).
AE1A6B9457F6E298 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAALQADLMNLRMELQSYRGSATPAAAKLLTPAAPRPHNSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEMBER 13.
CLEAVAGE (BY FURIN)
                                                MIM; bu44/4; -.
GO; GO:000824; P:positive regulation of cell
GO; GO:000165; P:signal transduction; TAS.
InterPro; IPR066052; TNF_family.
Pfam; PF00229; TNF; 1.
SMART; SM0207; TNF; 1.
PROSITE; PS00251; TNF 1; 1.
PROSITE; PS50049; TNF 2; 1.
CYtokine; Immune response; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Pred. No. 9.9e-
27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                410 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROCESSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ancient ubiquitous protein 1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Missing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J;
MEDLINE=96411699; PubMed=8812468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 40, Created)
(Rel. 40, Last seqn
(Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27433 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96
247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104
                                                                                                                                                                                                                                                                                                                                        Cytokine; Immune resp
Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104
196
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             the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 NSSRGHRNRR-----AFPGPEETEQDVDLSA------PPALRNIIQ-----DCLQ 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 MKRQRHPRLRPQSVQSSFPSPPSPSSDVQLTTLAHRVKEVLPHVPLNVIQRDLARTGCVD 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 STRLPPTPLLLPPEEEATNGREGLLRFSSWPFSIQDVVQPLTLVVSVTVSVTVSDASWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 SELLWSLFVPFTVYQVRWLHPIRRQLGEESBEFALRVQQLVAKELGQIGTRLTPADKAEH
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STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       58;
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Pseudomonadaceae, Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 SAKTLPPPCLCFCSEKGEDMKVG------YDPITPQKEEGAV---
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01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alginate biosynthesis transcriptional regulatory protein algB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92149314; PubMed=1738315;
Goldberg J.B., Dahnke T.;
"Pseudomonas aeruginosa AlgB, which modulates the expression
alginate, is a member of the NtrC subclass of prokaryotic
                                                                                                                                                                                                                                                                                                                                                                                                        / Match 6.9%; Score 83; DB 1; Length 410; Local Similarity 22.1%; Pred. No. 3.1; nes 44; Conservative 20; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                        38 410 ANCIENT UBIQUITOUS PROTEIN 1.
410 AA; 46121 MW; E7D070CEB296BD5B CRC64;
                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                         EMBL, U41736; AAC52839.1; -. MGD; MGI:107789; Aupl. InterPro; IPR002123; Acyltransferase. InterPro; IPR003892; CUE. Ffam; PP02845; CUE. SWART; SM00546; CUE; 1. SWART; SM00563; PISC; 1.
                                                                                                                                                                                                                                                                                                                      POTENTIAL
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STRAIN=Isolate FRD;
MEDLINE=91139582; PubMed=1899859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 LIADSDTPTIRKGTYTFVP 148
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen."; Nature 406:959-964(2000).

--- FONTION: POSITIVE REGULATOR OF ALGINATE BIOSYNTHETIC GENE (ALGD).
--- SIMILARITY: Contains 1 sigma-54 factor interaction ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 TLPPPCLCFCSEKGEDMKVGYDPIT------POKEEGAVLLSSSFTAMSLYQLAAL
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16 SIGMA-54 PACTOR INTERACTION (POTENTIAL).

18 ATP (POTENTIAL).

247 ATP (POTENTIAL).

445 H-T-H MOTIF (BY SIMILARITY).

49323 MW; E6452B88457CBC17 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGREMMS; TIGRO1199; HTH fis; 1.
PROSITE; PS0010; RESPONSE REGULATORY; 1.
PROSITE; PS00675; SIGMAS4 INTERACT 1; 1.
PROSITE; PS00689; SIGMAS4 INTERACT 2; 1.
PROSITE; PS00689; SIGMAS4 INTERACT 3; 1.
PROSITE; PS000699; SIGMAS4 INTERACT 4; 1.
Sensory transduction; Phosphorylation; Transcription regulation; DNA-binding; Activator; ATP-binding; Alginate biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.7%; Score 81; DB 1; Length 449; 25.7%; Pred. No. 5.3; ative 18; Mismatches 63; Indels
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EMBL; AR0499: A38449.
FIR; A38449; A38449.
HSSP; P41789; JNWR.
INTERPRO; IPR003593; AAA ATPABE.
INTERPRO; IPR003197; HTH_FIS.
INTERPRO; IPR003197; HTH_FIS.
INTERPRO; IPR003197; HTH_FIS.
INTERPRO; IPR003197; HTH_FIS.
FAMR; PF00394; HTH 8; 1.
Pfam; PF00364; HTH 8; 1.
Pfam; PF00158; Sigma54_activat; 1.
ProDon; PD000039; Response_reg; 1.
SMART; SM00382; AAA; 1.
SMART; SM00448; REC; 1.
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DOMAIN 10
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EF GTPbind

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R Pfam; PR03164; EFG_Lv; ...
R Pfam; PR03164; GTP_EFTU; 1.
R Pfam; PR03144; GTP_EFTU D2; 1.
DR PRINTS; PR001315; ELONGATNFCT.
DR TIGRFAMS; TIGR00231; SEACTOR GTP; 1.
DR ROSITE; PS00301; ERACTOR GTP; 1.
KW Elongation factor; Protein biosynthesis; GTP-binding.
FT NP_BIND 26 33 GTP (BY SIMILARITY).
FT NP_BIND 158 161 GTP (BY SIMILARITY).
FT NP_BIND 164 108 GTP (BY SIMILARITY).
FT NP_BIND 158 161 GTP (BY SIMILARITY).
FT NP_BIND 158 161 GTP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RA Wood V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A., Rajandram B., Baker S., Basham D., Bowman S., Ragouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Ragouros J., Brown D., Brown S., Chillingworth T., Churcher C.M., A Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., RA Holroyd S., Hornbaby T., Howarth S., McDonald S., McLean J., Annes L., Jones M., Lather S., McDonald S., McLean J., Ra Horrer S., McDonald S., McLean J., Rah Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., RA Oliver K., O'Neil S., Parsen D., Quail M.A., Rabbinowitsch E., Allenter S., Saunders R., Squares S., Stevens K., Asklton J., Squares R., Squares S., Stevens K., Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Rablor S., Volckaert G., Aert R., Roben J., Grymonprez B., Woddward J., Volckaert G., Aert R., Robert D., Hilbert H., Rabellon J., Slumermann W., Wedler H., Wambutt R., Pohl T.M., Rabel C., Fuchs M., Wedler H., Wambutt R., Purnelle B., Rager P., Zimmermann W., Wedler H., Wambutt R., Hunt C., Moore K., Hurs S., A Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Down T., McCoulle M.R., Sallsen I., Potashkin J., Rahbakovski G.V., Usseyt D., Barrell B.G., Nurse P., Marting A.R., Parlen I., Berlen B., R., The ganne sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN FROM THE A-SITE TO THE P-SITE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 415:871-8880(2002).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLOCATION OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THI RIBOSOWE (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mita K., Morimyo M., Ito K., Sugaya K., Bbihara K., Hongo B., Higashi T., Hirayama Y., Nakamura Y.; Comprehensive Cloning of Schizosaccharomyces pombe genes encoding translation elongation factors."; Gene 187:259-266(1997).
                           15-JUL-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Elongation factor 2 (FR-2).
(EFT1 OR SPCP31B10.07) AND (EFT2 OR SPAC513.01C OR SPAPYUK71.04C)
                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (EFT1 AND EFT2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97254480; PubMed=9099890;
      O14460; Q9USG7; Q9USZ9; Q9UT64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EF-G/EF-2 SUBFAMILY.
                                                                                                                                                                                                                                                                        Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4896;
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------CLQLIADSDTPTIRKGTYTFVPWLLSFKRGNALYSQVLYTDPIF----- 170 678 EENLRSCRFNILDVVLHAD--AIHRGGGQIIPTARRVVYASTLLASPIIQEPVFLVEIQV 735

127

---AMG---HVIQRKKVHVFGDE 187

-----AFPGPETEQD--VDLSAPPALRNIIQD------

101

516 PCVLCTTSESGEHIVAG-----AGELHLEIC-----LKDLQEDHAGIPLKISP

11 PC-LCFCSEKGEDMKVGYDPITPQKEEGAVLLSSSFTAMSLYQLAALQADLMNLRMELQ-

76; Indels 106;

28; Mismatches

53; Conservative

Score 80; DB 1; Length 842; Pred. No. 15;

6.6%; Score 80; 20.2%; Pred. No.

---SYRGSATPAAKLLTPAAPRPHNS--------SRGHRNRR-

69

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similarity).
-!- CATALYTIC ACTIVITY: L-histidinol + 2 NAD(+) + H(2)0 = L-histidine
                                                                                                                                                                                                                                                                                                                                                              Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D., Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M., Fleis M.W. B.J., Stlekema W., Klein Lankhorst R.M., Bron P.A., Hoffer S.M., Nierop Groom W.N., Kerkhoven R., De Vries M., Ursing I De Vos W.M., Siezen R.J.;

"Complete genome sequence of Lactobacillus plantarum WCFS1.";

Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995 (2003).

-!- FUNCTION: Catalyzes the sequential NAD-dependent oxidations of histidinal to L-histidine (By
                                                                                                                                                                                                                                         Bacteria, Firmicutes, Lactobacillales, Lactobacillaceae,
Lactobacillus.
                                                                                                                                 15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hishidinol dehydrogenase (EC 1.1.1.23) (HDH).
                                                                                                    428 AA
MEDLINE=22480296; PubMed=12566566;
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=NCIMB 8826 / WCFS1;
                                                                                                  STANDARD;
                                                                                                                                                                                                                           Lactobacillus plantarum.
                                                                                                                                                                                                                                                                              NCBI_TaxID=1590;
                                                                                                  HISX LACPL
P59399;
                                                                                    LACPL
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GeneDB_SPombe; SPAC513.01c; -. GeneDB_SPombe; SPCP31B10.07; -. AL121859; CAB58373.1; -. EMBL; D83976; BAA23591.1; -. EMBL; D83975; BAA23590.1; -. PIR; T41697; T41697

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genome sequence.";
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                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 VTPPQVDGINPAVLAAAKIAGVDAIYQVGGAQA-----IAALAYGTESIPAVDKIIGFG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1: | | | :: 1 | | 209 ----NIFVATAKKQVFGQVAIDMVAGPSEIGILADDSADPRQLAADLLSQAEHDRRARP 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 ILITDSADLAQAVSDNVTSQLK------VLPREAIATDAVNEKGFIAVV 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V. Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcook K., Basham D., Entilngworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Selton S., Squares R., Stelton S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 ITPQKEEG---AVLLSSSFTAM-SLYQLAALQADLMNLRMELQSYRGSATPAAAKLLTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 APRPHNSSRGHRNRRAF-----PGPEE-----TEQDVDLSAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 ALRNIIQDCLQLIADSDTPTIRKGTYTFVPWLLSFKRGNALYSQVLYTDPIFAMGHVIQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84; Indels 67; Gaps
                                                                                                                                                                                                                                                                                                                                            HAMAD; MF 01024; -; 1.
PROSITE; PS00611; HISOL_DEHYDROGENASE; FALSE_NEG.
Histidine biosynthesis; Oxidoreductase; NAD; Metal-binding; Zinc;
                                COFACTOR: Binds 1 zinc ion per subunit (By similarity). PATHWAY: Histidine biosynthesis; ninth (last) step. SIMILARITY: Belongs to the histidinol dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307 AKIEEMFDLMNTVA------PEHLEVQLKNPTQYLNLIKNAGSVFLG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 KKVHVFGDELSLVTLFRCIQNLEEGDEIQLAIPRENAQISRNGDDTFFG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 6.6%; Score 79.5; DB 1; Length 428; I Similarity 18.8%; Pred. No. 6.9; 43; Conservative 35; Mismatches 84; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                          ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protein-export membrane protein secD.
PSECD OR RVZ-897C OR MT2664 OR MTCY227.14.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           573 AA
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MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                      EMBL; AL935259; CAD64837.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45985 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           322
323
254
257
356
415
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428 AA;
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Best Local Similarity
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323
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Q50634;
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                                                     SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.P., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 IAQEKKLRQSTNQYMQMVALQFQATRCESDDILAGNDDPKLPLVTCSTDHKTAYLLAPSI
                                                                                                                                                                                                                                                                                   laboratory strains.",
Submitted (Apr-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN PROTEIN EXPORT.
-!- SUBMIT: PART OF THE PROKARAYOTIC PROTEIN TRANSLOCATION APPARATUS
-!- SUBMIT: PART OF THE PROKARAYOTIC PROTEIN TRANSLOCATION APPARATUS
WHICH COMPRISE SECA, SECB, SECB, SECE, SECF, SECG AND SECY
[EN SIMILARITY: DOCATION: Integral membrane protein (By similarity).
-!- SUBCELLULAR LOCATION: THE SECD/SECF FAMILY. SECD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                     "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57;
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TICRFRAMS; TICRO1129; SCCD; 1.
Protein transport; Translocation; Transmembrane; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
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PIR; B70726; B70726.
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InterPro; IPR005791; SecD.
InterPro; IPR003335; SecD_SecF.
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SHK1 RAT
D SHK1 RAT STANDARD; PS
AC Q9WV48; Q9QWU13; Q9WUE8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60267 MW;
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les 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z77724; CAB01256.1;
Nature 393:537-544 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33
405
430
461
509
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489
514
573 AA;
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TRANSMEM 13
TRANSMEM 385
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EMBL;
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    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
38-FEB-2003 (Rel. 41, Last annotation update)
38-FEB-2003 (Rel. 41, Last annotation protein (GKAP/SAPAP interacting protein) (SPAR interacting protein) (SSTR interacting protein)
                                                                                                                                                                                                       MEDLINE-99419021; PubMed=10488079;
Yao I., Hata Y., Hirao K., Deguchi M., Ide N., Takeuchi M., Takai Y.;
"Synamon, a novel neuronal protein interacting with synapse-associated protein 90/postsynaptic density-95-associated protein.";
J. Biol. Chem. 274:27463-27466(1999).
                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1 AND 3), AND INTERACTION WITH DIGAP1 AND
                                                                                                                                                                                                                                                                                                       STRAIN=Sprague-Dawley;
MEDLINE=99360650; PubMed=10433268;
Naisbitt S., Kim E., Tu J.C., Xiao B., Sala C., Valtschanoff J.,
Weinberg R.J., Worley P.F., Sheng M.;
"Shank, a novel family of postsynaptic density proteins that binds to
the NMDA receptor/PSD-95/GKAP complex and cortactin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99360651; PubMed-1043269;
Tu J.C., Xiao B., Naisbitt S., Yuan J.P., Petralia R.S., Brakeman P., Doan A., Aakalu V.K., Lanahan A.A., Shang M., Worley P.F.;
"Coupling of mGluk/Homer and PSD-95 complexes by the Shank family of postsynaptic density proteins.";
Neuron 23:583-592(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lim S., Naisbitt S., Yoon J., Hwang J.I., Suh P.G., Sheng M., Kim E., "Characterization of the Shank family of synaptic proteins. Multiple genes, alternative splicing, and differential expression in brain and
                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tobaben S., Suedhof T.C., Stahl B.; "The G protein-coupled receptor CL1 interacts directly with proteins of the shank family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20020275; PubMed=10551867;
Zitzer H., Hoenck H.-H., Baechner D., Richter D., Kreienkamp H.-J.;
"Somatostatin receptor interacting protein defines a novel family of
multidomain proteins present in human and rodent brain.";
J. Biol. Chem. 274:32997-33001(1999).
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Bockers T.M., Mameza M.G., Kreutz M.R., Bockmann J., Weise C.,
Buck F., Richter D., Gundelfinger B.D., Kreienkamp H.-J.;
"Synaptic scaffolding proteins in rat brain. Ankyrin repeats of
multidomain Shank protein family interact with the cytoskeletal
protein alpha-fodrin.";
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 4), AND INTERACTION WITH DLGAP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PARTIAL SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4 AND 5), AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [6]
INTERACTION WITH HOMER-1, AND SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARTIAL SEQUENCE FROM N.A. (ISOFORM 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol. Chem. 275:36204-36210(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 274:29510-29518(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 276:40104-40112(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20549637; PubMed=10958799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99436166; PubMed=10506216;
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERACTION WITH SPIANI
                                                                                                                                                                                                                                                                                                                                                                                        Neuron 23:569-582 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE.
                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            development.";
                                                                                                                                                                                            TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rissum=Brain;
                                                                                  SHANK1
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseaise.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sheng M., Kim E.;

"The Shank family of scaffold proteins.";

"The Shank family of scaffold proteins.";

"Cell Sci. 113:1851-1856(2000).

"Cell Sci. 113:1851-1856(2000).

"Cell Sci. 113:1851-1856(2000).

"Coll Sci. 113:1856(2000).

"Coll Sci. 113:186(2000).

"Coll Sci. 113:186(200).

"Coll Sci. 113:186(2000).

"Coll Sci. 113:186(2000).
"Coll Sci. 113:186(2000).
"Coll Sci. 113:186(2000).
"Coll Sci. 113:186(2000).
"Coll Sci. 113:186(2000).
"Coll Sci. 113:186(2000).
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TISSUE SPECIFICITY: Expressed only in brain (neuropil of cortex,
CA1 region hippocampus and molecular layer of cerebellum).
DEUELOPMENTAL STAGE: Expression increases from low levels at birth
to high levels at 3-4 weeks before dropping slightly in adulthood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expressed in the cortex and the molecular layer of the cerebellum at postnatal day 7. Isoform 2 expression does not change during developmment of both cortex and cerebellum. Isoform 4 expression
                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Cytoplasmic; postsynaptic density of neuronal cells. Colocalizes with alpha-latrotoxin receptor 1. ALTERNATIVE PRODUCTS:
MEDLINE=21389514; PubMed=11498055;
Sala C., Piech V., Wilson N.R., Passafaro M., Liu G., Sheng M.;
"Regulation of dendritic spine morphology and synaptic function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                decreases significantly during development of cortex but not
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--- SIMILARITY: BELONGS TO THE SHANK FAMILY.
--- SIMILARITY: Contains 7 ANK repeats.
--- SIMILARITY: Contains 1 PDZ/DHR domain.
--- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
--- SIMILARITY: Contains 1 SH3 domain.
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Comment=Additional isoforms seem to exist;
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                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20267867; PubMed=10806096;
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InterPro; IPR001478; PDZ.
InterPro; IPR001660; SAM.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                              Neuron 31:115-130(2001)
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                                                                                                                                                                                    Shank and Homer.
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15-JUL-1998 (Rel. 36,
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                                                                                                                                                                                                                                                                                                                   -> MALSAVGGGGGALPQPPPALSSSWPALGPRRRSVWY
IX (in isoform 2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAAKL-------LTPAAPRPHN
                                                                                                                                                                                                                                                                                                               SOEGROESRSDXAKRLFRHYTVGSYDSFDAPSLIDGIDSG
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LSEDSQTSLLSKPS -> QYRIVVKSSDFGDF (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 6.6%; Score 79.5; DB 1; Length 2167; Local Similarity 24.8%; Pred. No. 59; hes 40; Conservative 24; Mismatches 50; Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 S -> T (IN REF. 1).

S -> N (IN REF. 2).

R -> K (IN REF. 1).

A -> T (IN REF. 1).

S -> D (IN REF. 1).

S -> N (IN REF. 2).

3 MW, 3P478B5A7B18BA86 CRC64;
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                                                                           SMAKI; SMUJACO; OND; 1.

PROSITE; PSSOOMS; ANK_REPEAT; 3.

PROSITE; PSSOOMS; ANK_REP_REGION; 1.

PROSITE; PSSOOMS; SH3; 1.

PROSITE; PSSOIMS; SMA_DOMAIN; 1.

PROSITE; PSSOIMS; SMA_DOMAIN; 1.

REPEAT 195 210

ANK 1.

REPEAT 212 245

ANK 2.
                                                                                                                                                                                                                                                                                                                                              /FTId=VSP 006073.
Missing (In isoform 3).
/FTId=VSP_006074.
                                                                                                                                                                                                                                                                                                                                                                              (in isoform 4).
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Missing (In isoform 5)
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POLY-GLY.
POLY-PRO.
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ANK 4.
ANK 5.
ANK 6.
ANK 7.
SH3.
SPDZ.
SPDZ.
POLY-PRO.
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T160_HUMAN
ID T160 HUMAN STANDARD; PF
AC Q92993; O95624; Q13430; Q9BWK7;
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1174
11246
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AA; 226333 M
                              ProDom; PD000066; SH3; 1.
SMART; SM00248; ANK; 6.
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278
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                                                  SMART; SM00228; PDZ; 1.
SMART; SM00454; SAM; 1.
SMART; SM00326; SH3; 1.
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Pfam; PF00595; PDZ; 1.
Pfam; PF00536; SAM; 1.
Pfam; PF00018; SH3; 1.
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CONFLICT
SEQUENCE
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MEDLINE-22388257, PubMed=12477932;

MEDLINE-22388257, PubMed=12477932;

MEDLINE-22388257, PubMed=12477932;

MEDLINE-22388257, PubMed=12477932;

MEDLINE-22388257, PubMed=12477932;

MEDLINE-22388257, PubMed=12477932;

MAISTER R.D., Colling F.S., Wagner L., Sheamen C.M., Schuler G.D.,

Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wanja J., Haish F.,

MAISTER S. Morden H., Moore T., Max S.I., Wanja J., Haish F.,

Brownstein M.J., Usdin T.B., Forshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Milalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Butterfield Y.S.N., Zrzywinski M.I., Skalska W.,

Schnerch A., Schein J.E., Jones S.J.M., Marra W.A.;

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                "Identification of a cellular protein that specifically interacts with the essential cysteine region of the HIV-1 Tat transactivator."; Virology 216:357-366(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=12551922;
Xiao H., Chung J., Kao H.-Y., Yang Y.-C.;
Xiao H., Chung J., Kao H.-Y., Yang Y.-C.;
J. Biol. Chem. 278:11197-11204(2003)
-!- FUNCTION: Binds to the Tart protein of the human immunodeficiency virus (HIV). Specific binding of TIP60 to TAT might be an important feature for efficient TAT transactivation of HIV gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Interacts with HIV1 TAT, PLA2G4A/CPLA2, BDNRA and HDAC7 SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              þe
                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee H.-J., Chun M., Kandror K.V.; "Tip60 and HDAC7 interact with the endothelin receptor a and may
                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Fibroblast, and placenta;
MEDLINE-21309279; PubMed-11416127;
Sheridan A.M., Force T., Yoon H.J., O'Leary E., Choukroun G.,
Taheri M.R., Bonventre J.V.;
PLIP, a novel splice variant of Tip60, interacts with group IV
cytosolic phospholipase A(2), induces apoptosis, and potentiates
          15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
60 kbn Tat interactive protein (Tip60) (HIV-1 Tat interactive protein) (CPLA(2) interacting protein).
                                                                                                                                                                                                                                                                                                                                                                                                    (ISOFORM 2), INTERACTION WITH PLA2G4A, AND
                                                                                                                                                                                                                                                       MEDLINE-96182937; PubMed-8607265;
Kamine J., Elangovan B., Subramanian T., Coleman D.,
Chinnadurai G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse cDNA sequences.";
1. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 involved in downstream signaling.";
J. Biol. Chem. 276:16597-16600(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Cell. Biol. 21:4470-4481(2001).
                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prostaglandin production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERACTION WITH EDNRA.
PubMed=11262386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (: SUBCELLULAR LOCATION
                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                             rissum=Lymphoblast;
                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307 AEEDEELTSSÖLDNIEIEVV---GSPRPPASS-PPPPPRPHPRGRDHDHDHGHHRADDR 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 GPEETEQDVDLSAPPALRNIIQDCLQLIADSD---TPTIRKGTYTFVPWLLSFKRGNALY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363 GPQRHHR----LPPE-----PTFVSPSDIFVTPT---GS----PALLLGFLGSALA 402
                                                                                SEQUENCE FROM N.A.

MEDLINE=8513870'O; PubMed=2983115;
Rea T.J., Timmins J.G., Long G.W., Post L.E.;

"Mapping and sequence of the gene for the pseudorabies virus
"Mapping and sequence of the gene for the pseudorabies virus
Jycoproteain which accumulates in the medium of infected cells.";
J. Virol. 54:21-29(1985).
-I. SIMILARITY: TO EHV-1 GLYCOPROTEIN G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97305158; PubMed=9161424; Beakin W.J., Furniss C.S., Parker V.E., Shaw C.H.; Insolation and characterisation of a linked cluster of genes from Agrobacterium tumefaciens encoding proteins involved in flagellar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ( POTENTIAL).
( POTENTIAL).
( ) ( POTENTIAL).
( ) ( POTENTIAL).
( ) ( POTENTIAL).
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 36, Last annotation update)
Plagellar P-ring protein precursor (Basal body P-ring protein)
PLGI OR ATUG550 OR AGR C 970.
Agrobacterium tumefaciene (strain CSS / ATCC 33970)
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae: Rhizobium/Agrobacterium group; Agrobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    498 AA; 53721 MW; 17DEA180672A62DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 SQVLYTDPIFAMGHV--IQRKKVHV---FGDELSLVT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRPLHLTAGETAQHVREAQQKSRHIRSLGGLQLSVET 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73;
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(GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.5%; Score 78.5; Di
25.3%; Pred. No. 11;
:ive 26; Mismatches
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N-LINKED
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N-LINKED
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InterPro; IPR003363; Herpes_gG.
Pfam; PF02400; Herpes_gG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M10986; AAC35206.1; -.
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86
142
226
443
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Gene 189:135-137(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
tes 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=176299;
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                             NCBI TaxID=10350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein.
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLGI AGRT5
Q44340;
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Matches
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                             NA REPRESENTATION OF THE PRINCE OF THE PRINC
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                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibsib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 SGKTLPIPVQITLRFNLPKEREAIPGGEPDQP-----LSSS-----SCLQPNH 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 MNLRMELQSYRGSATPAAAKLLTPAAPRPHNSSR-----GHRNRRAFPGPEETEQDV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 DLSAPPA-------LRNIIQDCLQLIADSDTPTIRKGTYTFVPWLLSF 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 SDGIPSAPRMTGSLVSDRSHDDIVTRMKNI--ECIEL------GRHRLKPWYFS- 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 SAKTLPPP---CLCFCSEKGEDMKVGYDPITPOKEBGAVLLSSSFTAMSLYQLAALQADL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 RSTKRKVEVV-SPATPVPSE-TAPASVFQNGAARRAVAAQPGRKRKSNCLGTDEDSQDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 KRGNALYSQVLYTDPIFAMGHVIQRKKVHVFGDELSLVTLFRCIQ-NLEEGDEIQLAIPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0003713; F:transcription co-activator activity; TAE
GO; GO:0006366; P:transcription from Pol II promoter; TAS.
InterPro; IPR000933; Chromo.
InterPro; IPR002717; MCZ SAS.
Pfam; PF01853; MOZ_SAS; I.
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                                                                                                                                                                           Isoid=092993-2; Sequence=VSP 007438;
-!- SIMILARITY: BELONGS TO THE MYST (SAS/MOZ) FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           os.
Pseudorabies virus (strain Rice) (PRV).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (in isoform 2) P_007438.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuclear protein; Zinc-finger; Alternative splicing.
ZN FING 261 283 C2HC-TYPE (POTENTIAL).
VARSPLIC 96 147 Missing (in isoform 2)
                                                      Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
Secreted glycoprotein GX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.6%; Score 79; DB 1
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                                                                                                                IsoId=Q92993-1; Sequence=Displayed;
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U67734; AAD00163.1; -.
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MIM; 601409; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58581 MW;
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                                                                                                                                             Name=2; Synonyms=PLIP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U74667; AAB18236.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00298; CHROMO; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 23.2
1es 59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 3
513 AA;
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138 DGQIYAVAQGALIVNG-----FSAQGDAATLTQGVTTSARVPNGAIIERELPSKFKD 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92263758; PubMed=1316673; Colle C.F. III, Flowers C.C., O'Callaghan D.J.; Colle C.F. III, Flowers C.C., O'Callaghan D.J.; Colle C.F. III, Flowers encoding a protein kinase, homolog of glycoprotein gx of pseudorabies virus, and a novel glycoprotein map within the unique short segment of equine herpesvirus type 1."; Virology 188:545-557(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61;
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                    190 SVNĽVLOLRNPDFSTAVRVADVVNAFARARYGDPÍ--ÁEPRDSQEÍA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78; Indels
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                                                                                                                                                                                                                                                                                                                                                    Equine herpesvirus type 1 (strain Kentucky A) (EHV-1).
Viruses, dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                           01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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GLYCOPROTEIN.
SER/THR-RICH.
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SIGNAL 1 25 POTENTI
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Matches 43; Conservative
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383
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371
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                                             187 ELSLVTLFR----
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354 3
48 128 3
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CARBOHYD
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ID YAPI HI
AC P46937
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VGLZ HSVEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 IAAVMVTANLP-PF-----ASPG---SRVDVTVSSLGDATSLRGGNLIMTSLSGA 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 EKGEDMK-VGYDPITPQKEEGAVLLSSSFTAMSLYQLAALQADLMNLRMELQSYRGSATP 76
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                                                                                                                                                                                                                                                                                                                                                                                             38 QAĞRDNQLIĞYGLVVGLQGTĞDSLRSSPFTEQS-----MRAMLQNLGITTQGGQSNAKN
                      MEDLINE=21608550; PubMed=11743193;
Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland B., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
Sanang S., Yoo H., Tao Y., Biddle P., Jung M., Kreepan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56; Gaps
                                                                                                                                                                                                                                                                    "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROTATION.
SUBUNIT: THE BASAL BODY CONSTITUTES A MAJOR PORTION OF THE FLAGELLAR ORGANELLE AND CONSISTS OF FOUR RINGS (L, P, S, AND M) MOUNTED ON A CENTRAL ROD (BY SIMILARITY).
SUBCELLULAR LOCATION: Periplasmic (By similarity).
SIMILARITY: Belongs to the flg1 family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 373;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLAGELLAR P-RING PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=21608551, PubMed=11743194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP, MF_00416, -; 1.
InterPro; IRRO01182; Flag_FlgI.
PRO119; FlgI; 1.
PRINTS; PR01010; FLGPRINGFLGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Flagella; Periplasmic; Signal;
SIGNAL 1 26 PC
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                                                                                                                                                                                                                                                                                                               Science 294:2317-2323(2001).
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PIR; A12643; A12643.
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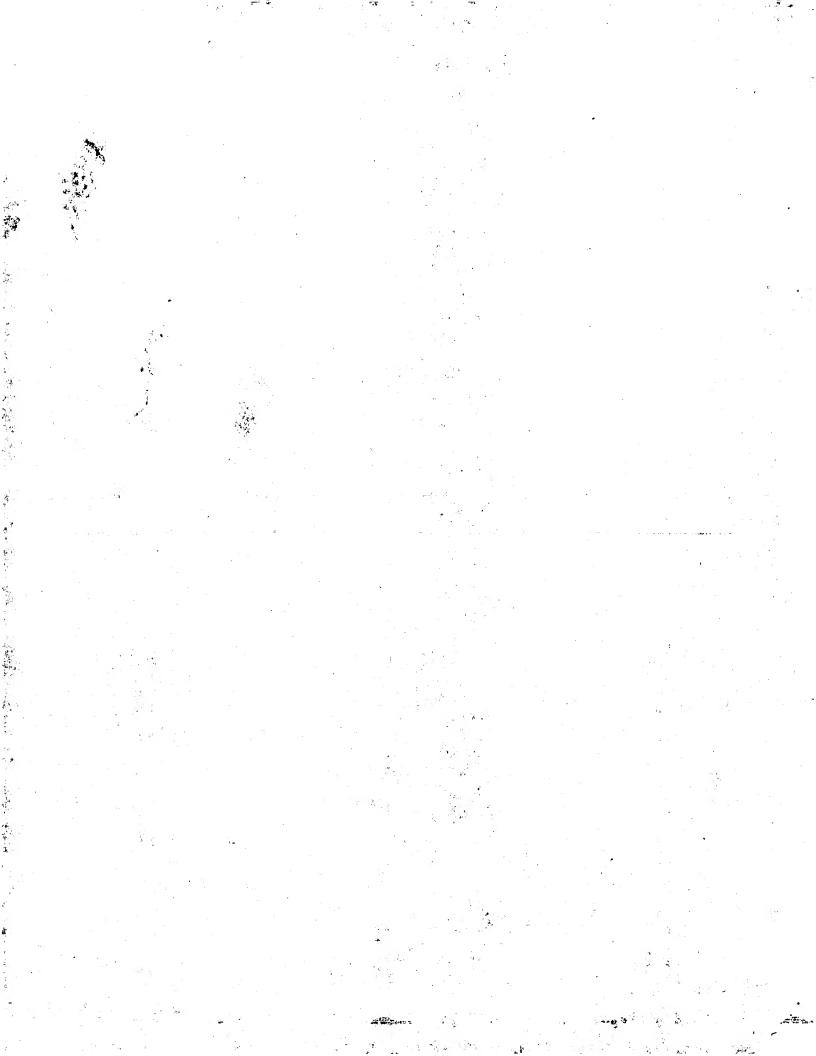
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERACTION WITH WBP1 AND WBP2.

MEDLINE=97347517; PubMed=2202023;
Chen H.I., Einbond A., Kwak S.-J., Linn H., Koepf E., Peterson S.,
Kelly J.W., Sudol M.;
"Characterization of the WW domain of human Yes-associated protein and
its polyproline containing ligands.";
J. Biol. Chem. 272:17070-1777(1997);
-i- SUBUNIT: Binds to the SH3 domain of the YES kinase. Binds to WBP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37; Gaps
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MEDLINE=95301570; PubMed=7782338;
MEDLINE=95301570; PubMed=7782338;
Sudol M., Bork P., Einbond A., Kastury K., Druck T., Negrini M.,
Huebner K., Lehman D.;
"Characterization of the mammalian YAP (Yes-associated protein) gene
and its role in defining a novel protein module, the WW domain.";
J. Biol. Chem. 270:14733-14741(1995).
                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
DT 01-NOV-1995 (Rel. 32, Created)
DT 10-SNOV-1995 (Rel. 32, Late sequence update)
DE 15-SP-2003 (Rel. 32, Late sequence update)
DE 16-SP-2003 (Rel. 32, Late sequence update)
DE S. XDa Yea-associated procein (YAP65).

OS Homo sapiens (Human).

OC BUKATYCHAN PARADA (CARADA CARADA CAR
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Search completed: February 3, 2004, 07:44:16 Job time: 11.7956 secs



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66 NSSRGHRINRARAFQGPEETEQDVDLSAPPAPCLPGCRHSQHDDNGMNLRNIIQDCLQLIAD 125
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Q9HA87 Q9HA87 homo sapien Q9HCG0 Q9HGG0 homo sapien Q9G513 Q9F677 chloroflexu Q9L215 Q9E513 bifidobacte Q91215 Q91215 oncorbynchu Q8EM22 Q8EM22 bacteriobha P95190 Mycobacteri Q9UPW8 Q07386 lactococcus Q8UX74 Q8HZ7 arabidopsis Q8UX74 Q8HZ7 arabidopsis Q8UX18 Q8U365 caenorhabdi Q8VM13 Q8U365 caenorhabdi Q8X016 Q8V10 Q8X17 Q8C10 Q8X18 Q8C10 Q8X18 Q8C10 Q8X18 Q8C10 Q8C1A2 Q8C10 Q8C1A2 Q8C10 Q8C1A2 Q8C10 Q8C1A2 Q8C10 Q9BX4 Q8C10 <th>ALIGNMENTS</th> <th>PRT; 258 AA.</th> <th>Created) Last sequence update) Last annotation update)</th> <th>Craniata; Vertebrata; Buteleostomi; Sciurognathi; Muridae; Murinae; Mus.</th> <th>phalon; 351;</th> <th>ration Research Group Phase I & II Team; transcriptome based on functional annotation of As.";)).</th> <th>11FE93E782810 CRC64;</th> <th>Score 909; DB 11; Length 258; Pred. No. 7.1e-83; // Mismatches 1; Indels 60; Gaps 4</th> <th>SSSFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAAKLLTPAAPRPH 90</th> <th>LLSSSFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAAGAPELTAGVKLLTPAAPRPH 65</th>	ALIGNMENTS	PRT; 258 AA.	Created) Last sequence update) Last annotation update)	Craniata; Vertebrata; Buteleostomi; Sciurognathi; Muridae; Murinae; Mus.	phalon; 351;	ration Research Group Phase I & II Team; transcriptome based on functional annotation of As.";)).	11FE93E782810 CRC64;	Score 909; DB 11; Length 258; Pred. No. 7.1e-83; // Mismatches 1; Indels 60; Gaps 4	SSSFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAAKLLTPAAPRPH 90	LLSSSFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAAGAPELTAGVKLLTPAAPRPH 65
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SDTPTIRKGTYTFVPWLLSFKRGNALEEKENKIVVRQTGYFFIYSQVLYTDPIFAMGHVI 185
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                                    SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAA------KLLTPAAPRPHNSSR
                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUB=Liver;
MEDLINE=22354683; PubMed=12466851;
The FANYOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
BEMBL; ARO50384; BAC34225.1; --
SEQUENCE 199 AA; 21654 MW; 39392021D4EFD320 CRC64;
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Tumor necrosis factor.
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Pred. No. 1.7e-59;
1; Mismatches 2
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STRAIN=C57BL/6J; TISSUE=Urinary bladder;
MEDLINE=22354683; PubMed=12466851;
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                       ORKKVHVFGDELSLVTLFRCIQN
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Best Local Similarity 75.3%;
Matches 140; Conservative
                                                                     NGDDTFFGALKLL 232
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Q8BVA3
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the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK079180; BAC37571.1; -.
SEQUENCE 194 AA; 20961 MW; 85FCF3495B138377 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 44 SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAA------KLLTPAAPRPHNSSR
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                                                                                                                                                                                                     43;
                                                                                                                                                       Score 673.5; DB 11; Length 194; Pred. No. 2e-59; 0; Mismatches 2; Indels 43;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
NCBI_TaxID=9606;
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Gao H., He F., Li R.;

Gao H., He F., Li R.;

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

EMBL;

XY129226; AAN08422.1; -.

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SEQUENCE 208 AA; 22767 MW; EEA31D227033AA53 CRC64;
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Last annotation update)
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89 PHNSSRGHRNRRAFPGPEETEQ-DVDL------SAPPALRNIIQDCLQLIADSDTP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 TIRKGTYTFVPWLLSFKRGNAL------YSQVLYTDPIFAMGHVIQRKK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220 AHVFGDDLSLVTLFRCIQNMPQSYPNNSCYTAGIAKLEBGDELQLTIPRRRAKISLDGDG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUE=Retina; MEDLINE=22354683; PubMed=12466851; The FANTOM Consortium, The FANTOM Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 AVLLSSSFTAMSLYQLAALQADLMNLRMELQSYRGSA-----TPAAAKLLTPAAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 AMLLSSCLAAVSLYHAITLKTELEALRSEL-IYRVRARSPLEQPPVSPGDKKAGASVSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 IQQKDDSSIVPWLLSFKRGTALEEQGNKIVIKETGYFFIYGQVLYTDTTFAMGHLIQRKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----LEEGDEIQLAIPRENAQISRNGDD
                                                                                                                                                                                                                                      Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                             "A chicken homolog of the B cell activating factor of the TNF family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.8%; Score 430.5; DB 13; Length 288; 43.4%; Pred. No. 8.1e-35; ive 21; Mismatches 65; Indels 55;
109 MPETLPNNSCYSAGIAKLEEGDELQLTIPRENAQISLDGDVTFFGALKLL
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Schneider K., Kolthow S., Schneider P., Goebel T., Kaspers
Staeheli P.,
                                                                                                                                                                                                                                                                                                                                                                                               (BAFF).";
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF506010; AAM90951.2; -.
SEQUENCE 288 AA; 31629 MW; 8E2F291D2495BB79 CRC64;
                                                                                                                                  01-OCT-2002 (TrEMBLrel. 22, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
TNF family B cell activation factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        410 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 VHVFGDELSLVTLFRCION-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 43.4%
Matches 108; Conservative
                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                         Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFFGALKLL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 TFFGAVRLL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor necrosis factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                         Gallus.
NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003
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01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Q8BXS2;
                                                                                                   Q8JHJ4
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                                                                     RESULT 7
                                                                                       Q8JHJ4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----YSQVLYTDPIFAMGHVIQRKKVHVFGDELSLVTLFRCIQN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . ||:|| ||||||
. 3 RNKRAVQAPEET-------VTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRG 48
                                                                                                                                                                                                                                                                                                                                                                                                                 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 RNRRAFPGPEETEQDVDLSAPPALRNIIQDCLQLIADSDTPTIRKGTYTFVPWLLSFKRG
                                                                                                                                                                                                                                                                                                                                                                                 80 KLLTPAAPRPHNSSRGHRNRRAFPGPEETEQDVDLSAPPALRNIIQDCLQLIADSDTPTI
                                                                                                                                                                                                                                                                                                                                                                                                    ---LEEGDEIQLAIPRENAQISRNGDDTF
                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                               48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48;
                                                                                                                                                                                                                                                                                                           Query Match
43.4%; Score 522; DB 4; Length 174;
Best Local Similarity 58.8%; Pred. No. 2.8e-44;
Matches 110; Conservative 12; Mismatches 17; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.7%; Score 490; DB 4; Length 158
60.6%; Pred. No. 3.9e-41;
... wismatches 9; Indels
                                                                                                                                                                                                  He F., Gao H., Li R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY129227; AAN08423.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
He F., Gao H., Li R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY129228, AM08424.1, -.
NON_TER 1
                                                                                                                                                                                                                                                                           SEQUENCE 174 AA; 19479 MW; 1AEBD4F2862EB3E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 158 AA; 17826 MW; 8346BCC0D333DCAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B-lymphocyte stimulator (Fragment). TNPSF13B.
          01-MAR.2003 (TrEMBLrel. 23, Create 01-MAR.2003 (TrEMBLrel. 23, Last so 01-MAR.2003 (TrEMBLrel. 23, Last an B-lymphocyte stimulator (Fragment) TNPSF138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 VFGDELSLVTLFRCIQN------
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Best Local Similarity 60.6
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FGALKLL 232
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                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                     NCBI_TaxID=9606;
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01-NOV-1996
01-NOV-1996
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Q13876;
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Q13876
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                                                                                                                                                                                                                                                                                                     261
                                                                                                                                                                                                                                                                                                                                                           98 NRRAFPGPEETEQDVDLSAPPALRNIIQDCLQLIADSDTPTIRKGTYTFVPWLLSFKRGN 157
                                                                                                                                                                                                                                                                                                                                                                                                      262 RRRAVLTQKHKKKKHSVLHLVPV--NITSK-----ADSDV-----TEVMWQPVLRRGR 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---LYSQVLYTDPIFAMGHVIQRKKVHVFGDELSLVTLFRCIQ-- 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307 GLEAQGDIVRVWDTGIYLLYSQVLFHDVTFTWGQVVSRE-----GQGRRETLFRCIRSM 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 LAALQADLMNLRMELQSYRGSATPAAAKLLTPAAPRPHNSS------RGHRNRRAFP 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------LYSQVLYIDPIFAMGHVIQRKKVHVFGDELSLVTLFRCIQ----- 198
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                                                                                                                                                                                                                                                                                                 207 ÓLRLCÓTELÓSLRREVSRLORSGGPSOKO----GERPWOSLWEOSPDVLEAWKDGAKSR
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                                                                                                                                                                                    Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KOYAMA T., TSUKAMOLO H., MASUMOLO K., Himeji D., HAYASHi K., Harada M., HOTJUCHI T., "Genomic Structure of APRIL, a proliferation-inducing ligand."; "Genomic Structure of APRIL, a proliferation-inducing ligand."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AF513501; AAM47279.1; -.

Interpro; IPR06605; TNF_family.

PROSITE; SM00207; TNF; 1.

SMART; SM00207; TNF; 1.

PROSITE; PS050049; TNF_1; 1.

PROSITE; PS050049; TNF_2; 1.

SEQUENCE 250 AA; 27453 MM; AE1E4FDEFD578898 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 PSDPDRAYNSCYSAGVFHLHQGDIITVKIPRANAKLSLSPHGTFLGFVKL 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199 -------NLEEGDEIQLAIPRENAQISRNGDDTFFGALKL 231
                                                                                                                                                                                 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                    Indels
                                                                                                                          Length
                                                                                                                                                                                                                                           52 QLAALQADLMNLRMELQSYRGSATPAAAKLLTPAAPRPHNS----
Nature 420:563-573(2002).
EMBL; AKO44387; BAC31897.1; -.
SEQUENCE 410 AA; 45881 MW; 590A4B74C33FB8D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                       th 12.6%; Score 152; DB 11; 1 Similarity 27.0%; Pred. No. 1.1e-06; 62; Conservative 22; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proliferation-inducing ligand APRIL.
Homo sapiens (Human).
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01-MAR-2003 (TrEMBLrel
                                                                                                                   Query Match
Best Local Similarity
Matches 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 A----
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                                                                                                                                                                                                                                                                                                                                                                                                                                           "An endogenous hybrid mRNA encodes TWE-PRIL, a functional cell surface TWEAK-APRIL fusion protein."; EMBO J. 21:5711-5720(5002). EMBO J. 21:5711-5720(5002). SEQUENCE 330 Aa; 36588 MW; PC6F3BCA29C029AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               274 PRCIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARAKLNLSPHGTFLGFVKL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 NSSRGHRNRRAFPGPEETEQDVDLSAPPALRNIIQDCLQLIADSDTPTIRKGTYTFVPWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 PITPQKEEGAVLLSSSFTAMSLYQL-----AALQADLMNLRMELQSYRGSATPAAAKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRCIQ-------NLEEGDEIQLAIPRENAQISRNGDDTFFGALKL
                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
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"Molecular cloning and expression of A novel bone-derived growth factor from a human osteosarcoma cell line.";
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; 142379; AAA89173.1; -.
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                                                                                                                                                                                                                                                                                                                                    MEDLINE-22299924; PubMed=12411489;
Pradet-Balade B., Medema J.P., Lopez-Fraga M., Lozano J.C.,
Kolfschoten G.M., Picard A., Martinez-A C., Garcia-Sanz J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.5%; Score 127; DB 4; Length 330; 27.1%; Pred. No. 0.00027; Live 21; Mismatches 50; Indels
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                 Last sequence update)
Last annotation update)
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Last annotation update)
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330 AA
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                                                    Created)
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InterPro; IPR0006663; Thiored.
InterPro; IPR006663; Thioredox_dom2
Pfam; PP00085; thiored; 1.
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                                                 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2003 (TrEMBLrel. 23,
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 LSFKRGNA----
                                                                                                                                                                Homo sapiens (Human)
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83 -TPAAPRPHNSSRG------HRNRRAFPGPE------ETEQDVDLS----- 115
                                                               588 KSPTNTTPHVPAEGPEASRPPKLHPGLRAAPGQEPPEHMADVQRNEQDEPLGQWHLRSET 647
                                                                                           116 -----APPALRNIIQDCLQLIADSDTPTIRKGTYTFVP--WLLSFK------RGNALY 160
                                                                                                                     648 QGLHCWLSPGLRRTASGALW------RSGAWAAAPSSWSTSLRPAGGPSWTGRGQW 697
                                                                                                                                                 161 SQV-------LYTDPIFAMGHVIQRKKVHVF-GDELSLVTLFRCIQNLEEGD 204
                                                                                                                                                                   Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
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MEDLINE-21996410; PubMed=12000953;
BEDLINE-21996410; PubMed=12000953;
BEDLINE-21996410; PubMed=12000953;
BEDLINE-21996410; PubMed=12000953;
BEDLINE-21996410; PubMed=1.0. Chanland G.L.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Wurphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandram M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR001128; Cytochrome_P450.
Pfam, PF00067; p450; J.
Hypothetical protein; Complete proteome.
SEQUENCE 420 AA; 45888 MW; F7FE250A4895A640 CRC64;
                                                                                                                                                                                                                                                                                                                                           Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                      420 AA
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                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                       205 EIQLAIPRENAQISRN 220
                                                                                                                                                                                                                                 752 E----AGEGAAISRH 762
                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 417:141-147(2002)
                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=A3(2);
Seeger K.J., Harris D.;
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62 NIRMELOSYRGSATPAAAKILTPAAPRPHNSSRGHRNRRAFPGPEETEODVDLSAPPALR 121
                                                                                                                        189 DLRISLDAAEGD-DPVAA--YTRVGERIHQLVRHKRER---PGPDVTSRMLTHPAGLTDE 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y., Nadai R., Sugano S., Aotsuka S., Yoshikawa Y., Nataunawa T., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Natamura Y., Nagahari K., Masuho Y., Sasaki N.; Submitca DNA sequencing project."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                  122 NIIQDCLQLIADSDTPTIRKGTYTFVPWLLSFKRGNALYSQVLYTDPIFAMGHVIQRKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 EKGEDMKVGYDPITPQ-----KEEGAVLLSSSFTAMSLYQLAALQADLMNLRMELQ
                                         Gaps
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Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Otagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 SYRGSATPAAAKLLTPAAPRPHNSSRG-----HRNRRAFPGPEETEQDVDLSAP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                       30;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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                                       Indels
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DB 16;
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                                       16; Mismatches
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6.1%; Pred. No.
7.4%; Score 89;
29.5%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein FLJ10826. Homo sapiens (Human).
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Homo sapiens (Human).
Query Match
Best Local Similarity 29.5
Matches 38; Conservative
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Matches 30; Conser
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26; Gaps . 4;
                                                                                                                                                                                                                                                                                                                        18 EKGEDMKVGYDPITPQ-----KEEGAVLLSSSFTAMSLYQLAALQADLMNLRMELQ 68
                                                                                                                                                                                                                                                                                              18 EKGEDMKVGYDPITPQ-----KEEGAVLLSSSFTAMSLYQLAALQADLMNLRMELQ 68
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamateu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T.; "NEDO human cDNA sequencing project."; "NEDO human cDNA sequencing project."; Submitted (AGG-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AR024314; BABL14880.1; -.. Hypothetical protein. SEQUENCE 402 AA; 46789 MW; OD62A85B40B9AC33 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                           244 T-----TDITEEGTSHSPPEPENNQMAISNNSQQSNEQTDPEPEENETKKESSVP 293
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080543;

01-OCT-2002 (TrEMBLrel. 22, Created)

01-OCT-2002 (TrEMBLrel. 23, Last sequence update)

01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

Hypotherical protein FLJ10826.

Hypotherical protein FLJ10826.

Hypotherical protein FLJ10826.

Bukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                            Query Match 7.3%; Score 88; DB 4; Length 402; Best Local Similarity 26.1%; Pred. No. 2.8; Matches 30; Conservative 17; Mismatches 42; Indels
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7.3%; Score 88; DB 4; Length 542;
Best Local Similarity 26.1%; Pred. No. 4.2;
Matches 30; Conservative 17; Mismatches 42; Indels
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Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC032919; AAH32919.1; -.
InterPro; IPR006620; Pro_4_hyd_alph.
SMART; SM00702; P4Hc; 1.
Hypothetical protein.
SEQUENCE 542 AA; 63246 MW; 8834BB200D5DBDB5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Q8N543
      SOWERER
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Search completed: February 3, 2004, 07:46:52 Job time : 32.9333 secs Mouse BAFF protein Mouse Neutrokine-a Murine B lymphocyt Human BLyS binding Murine B Lymphocyt

Mouse Neutrokine-a Mouse Neutrokine-a

Mouse neutrokine-a
Rat B lymphocyte s
Human Buys binding
Rat B lymphocyte s
Human Tamphocyte s

Amino acid sequenc Amino acid sequenc Amino acid sequenc Human TALL-I prote Human tumour necro

Human BAFF protein Human PRO738 polyp Human TACI-ligand

J O 6.4

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TNF; membrane bound; tumour necrosis factor ligand; D7; trimer; NF-kappa-B; modulator; CD40 inducer; gene therapy; vaccine; adjuvant; cytostatic; immunosuppressive; antibacterial; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266
/note= "Potential N-linked glycosylation site"
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/label= Transmembrane_domain
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ABJ00721
ABJ00721
ABG33582
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ABJ00722
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ABJ00722
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AAW73043
AAW73043
AAW828221
AAW82853
AAW3688
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(GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunomodulator.
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Domain
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 Membrane bound mur
Mouse Neutrokine-a
Murine B Lymphocyt
Human BLyS binding
Murine B Lymphocyt
Mouse Neutrokine-a
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Murine Kay-ligand.
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                                                                                               February 3, 2004, 07:43:37; Search time 38.6667 Seconds (without alignments) 952.359 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                        A Geneseq 19Jun03:*

| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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Compugen Ltd.
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               GenCore version (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
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ABG96469
ABJ00717
ABF47219
ABG33578
AAU79147
AAU10943
AAB08262
AAY04393
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Score

Result No.

Post-processing:

Database :

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Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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                                                                                                                                                                                  ligand, DT. DT or trimers are useful in immunotherapy or treatment of cancer. DT is useful against viral diseases or infections, or as a vaccine adjuvant. It may also be used as an immunogen to produce antibodies or for screening mechods, e.g. for identifying modulators of D7-receptor interaction. Modulators are useful for immunotherapy, particularly, in treating inflammation, autoimmune disease, other diseases associated with activation of transcription factor NF-kappa-B (e.g. rheumatoid arthritis, neuronal inflammation, asthma), cancers, infections (e.g. septic shock), or atherosclerosis. The D7 gene is useful ingent therapy, and may be employed for producing the protein by recombinant techniques. D7 antibodies are useful for locating the protein in a tissue, or for purifying the protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       77; Gaps
                                                                                 New member of the tumor necrosis factor ligand family, known as the ligand, useful in treating cancer, autoimmune disease or diseases associated with the activation of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                           21; Length 309;
                                                                                                                                                                         membrane bound murine tumour necrosis factor (TNF)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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7
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Pred. No. 3.2e-116;
0; Mismatches 2;
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             Kitson JDA, Winder AJ;
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                                                                                                                                           Disclosure, Fig 6, 48pp; English
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Best Local Similarity 74.4%;
Matches 230; Conservative
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            Farrow SN, Kaptein A,
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                                          2000-452393/39.
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                                                        N-PSDB; AAA51863
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ઠે g ઠ 셤 ઠે 셤 8 셤 ઠે 유 à 셤

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The invention relates to an isolated antibody (I) or its portion that specifically binds to a 285 residue neutrokine-alpha protein sequence or a 250 residue APRIL (proliferation inducing) ligand) polypeptide concentrate (S2). Also included are: (1) an antibody or its portion that competitively inhibits the specific binding of (I) by at least 50 or competitively inhibits the specific binding of (I) by at least 50 or competitively inhibits the specific binding of (I) by at least 50 or competitively inhibits the specific binding of (I) by at least 50 or competitively inhibits the nucleic acid, (4) a host cell comprising the nucleic acid, (7) a vector and information for treating disease or disorder such as autoimmune diseases, systemic lupus erythematosus, rheumatoid arthritis, systemia, multiple myeloma, Hodgkin's Iymphoma and non-Hodgkin's lymphoma, an immunodeficiency, hypo or hypergammaglobulinaemia, cheumatic heart disease, disease, myasthenia gravis, autoimmune competities, syndrome, Graves' disease, myasthenia gravis, autoimmune competities, primary chemolytic anaemia, infertility, chronic active hepatitis, primary chaemolity circlesis, other disorders such as inflammatory skin diseases including psoriasis, allergic conditions, atherosclerosis, antigen-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an
Graves' disease; myasthenia gravis; autoimmune haemolytic anaemia; infertility; chronic active hepatitis; primary biliary cirrhosis; inflammatory skin disease; psoriagis; allergy; atherosclerosis;
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                                                                                                              autoimmune thrombocytopaenia; antibody; chromosome 13q34
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990S-1269PP
990S-12699P
990S-130412P
990S-130696P
990S-131673P
990S-13673P
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99US-168624P.
99US-171108P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 TIRKGTYTFVPWLLSFKRGNALEEKENKIVVRQTGYFFIYSQVLYTDPIFAMGHVIQRKK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B lymphocyte stimulator protein binding protein; BLyS; immune disease; allergy; proliferative disease; infectious disease; arteriosclerosis; inflammatory disorder; hypergammaglobulinaemia; blood clotting; ischaemia; graft-versus-host disease; neurodegenerative disease; immunosuppressive; nephrotropic; antirheumatic; antiarthritic; neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV; antiasthmatic; antiallergic; thyromimetic; antianaemic; haemostatic; dermatclogical; antialfammacry; cardiant; ophthalmological; uropathic; antidiabetic; antithyroid; antidepressant; hepatotropic.
             antibody is also useful for diagnosing the disease or disorder, by sassaying expression of Neutrokine-alpha and APRIL expression level, in cells or body fluid of an individual and comparing the levels with a standard expression level, where an increase or decrease in the assayed Neutrokine-alpha and APRIL expression level compared to the standard expression level in indicative of a disease or disorder. The antibody is also useful for reducing or stimulating immunoglobulin production and to inhibit or stimulate proliferation of a cell of haematopoietic origin, preferably a B cell. The gene for Neutrokine-alpha is located on chromosome 13q34. The present sequence is a non-human Neutrokine-alpha
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complex mediated diseases and autoimmune thrombocytopaenia. The
                                                                                                                                                                                                                                                                                                                                                                            YSOVLYTDPIFAMGHVIORKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----LEEGDEIQLAIPRENAQISRNGDD
                                                                                                                                                                                                                                                                                                                                                                                                                          44 SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAA------KLLTPAAPRPHNSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GHRNRRAFFGPEETEQDVDLSAPPA---------LRNI I QDCLQLIADSDTP
                                                                                                                                                                                                                                                                            DB 23; Length 309;
                                                                                                                                                                                                                                                                                                                                                   1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPITPQKEEGA--
                                                                                                                                                                                                                                                                          Score 1103.5; DB 23
Pred. No. 3.2e-116;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine B lymphocyte stimulator protein #1.
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74.48;
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                                                                                                                                                                                                                                                                                            Local Similarity 74.4
les 230; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 TFFGALKLL 232
                                                                                                                                                                                                                                        309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-SEP-2002
                                                                                                                                                                                                                                          Sequence
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ABJ00717
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The present invention relates to the treatment, prevention or amelioration of a disease or disorder associated with: aberrant B hyphocyte stimulator (BLVS), BLyS receptor expression or activity; cells of haematopoietic origin; or proliferative disease; and reducing, inhibiting or stimulating immunoglobulin production, B cell proliferation and graft rejection involving administration of BLyS binding polypeptides are used in the treatment, prevention or amelioration of diseases such as immune system diseases, proliferative diseases, diseases of cells of hematopoietic origin, graft rejection, allergies infectious diseases, arteriosclerosis, inflammatory disorders, hypergammaglobulinaemia, blood clotting disorders, ischaemia, and neurodegenerative diseases. The present sequence is a B lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GHRNRRAFYGGPEETEQDVDLSAPPAPCLPGCRHSQHDDNGMNLRNIIQDCLQLIADSDTP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----YSQVLYTDPIFAMGHVIQRKK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 VHVFGDELSLYTLFRCIQNMPKTLPNNSCYSAGIARLEEGDEIQLAIPRENAQISRNGDD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tummour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunedeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94
                                                                                                                   The treatment of various diseases e.g. rheumatoid arthritis, comprises administering B Lymphocyte stimulator binding polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAA-.----KLLTPAAPRPHNSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GHRINRRAFPGPEETEQDVDLSAPPA--------LRNIIQDCLQLIADSDTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIRKGTYTFVPWLLSFKRGNALEEKENKIVVRQTGYFFIYSQVLYTDPIFAMGHVIQRKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1103.5; DB 23; Length 309;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 3.2e-116;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPITPQKEEGA--
                                                 Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human BLyS binding scFv VH CDR3 SEQ ID 3230.
                                                                                                                                                                         Disclosure; Page 304-306; 387pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP47219 standard; Protein; 309 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 230; Conservative
                (HUMA-) HUMAN GENOME SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232
                                                                                                                                                                                                                                                                                                                                                                                                                         stimulator protein.
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181 VHVFGDELSLVTLFRCIQN-------LEEGDEIQLAIPRENAQISRNGDD 223
                                                                                                                                                                                                                                                                                                                                             B Lymphocyte Stimulator protein; B Lymphocyte Stimulator binding peptide;
BLyS; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
synovial fluid; saliva; mucus; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a B Lymphocyte Stimulator (BLyS) binding polypeptide. BLyS binding peptides bind BLyS or BLyS-like proteins reversibly or irreversibly. The binding peptides are used in detection, isolation and/or purification of BLyS in a solution such as water or a buffer solution, as well as any fluid and/or cell obtained from an individual biological fluid, body tissue, body cell, cell line, tissue culture or other source containing BLyS or BLyS-like polypeptides. The biological fluids include sera, plasma, lymph, blood, blood fraction, urine, synovial fluid, spinal fluid, saliva and mucous. Sequences ABG33578 and ABG33579 represent murine B Lymphocyte Stimulator proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAA------KLLTPAAPRPHNSSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New B-lymphocyte stimulator binding polypeptide useful in detecting isolating BLyS or BLyS-like polypeptide comprises a specified amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                              Murine B Lymphocyte Stimulator (BLyS) protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1103.5; DB 23
Pred. No. 3.2e-116;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fleming TJ, Ladner RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPITPQKEEGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 186-188; 269pp; English.
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                                                                                                                                   ABG33578 standard; Protein; 309 AA
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Matches 230; Conservative
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301 TFFGALKLL 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2002
                                                                                                                                                                                         ABG33578;
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                                                                              RESULT 5
ABG33578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression administered to treat diseases associated with aberrant BLyS expression diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (CVID) and control of the con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAAGAPELTAGVKLLTPAAPRPHNSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 TIRKGTYTFVPWLLSFKRGNALEEKENKIVVRQTGYFFIYSQVLYTDPIFAMGHVIQRKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPITPQKEEGA--------VLLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAA-----KLLTPAAPRPHNSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---LRNIIQDCLOLIADSDTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----YSQVLYTDPIFAMGHVIQRKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VHVFGDELSLVTLFRCIQN--------LEEGDEIQLAIPRENAQISRNGDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 23; Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibodies against B Lymphocyte Stimulating polypeptides, us
the diagnosis and treatment of cancers and immune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1103.5; DB 23
Pred. No. 3.2e-116;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 3140-3141; 3148pp; English
                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.78;
74.48;
                                                                                                                                                                                                                                                                  17-0CT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                                                                                         15-JUN-2001; 2001WO-US19110
                                                                                                                                                                                                                                           16-JUN-2000; 2000US-212210P
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Matches 230; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-114799/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the invention.
                                                                                 WO200202641-A1.
                            Homo sapiens
                                                                                                                                   10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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120 137 180 180 240

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Gaps

77;

DB 23; Length 309;

Pred. No. 3.2e-116;

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Score 1103.5;

43 9 94 137

223

---LEEGDEIQLAIPRENAQISRNGDD

AAU79147

RESULT

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61 SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAAGAPELTAGVKLJTPAAPRPHNSSR 120
                                                                                                                                                                                                                                                                                                                    121 GHRNRRAFQGPEETEQDVDLSAPPAPCLPGCRHSQHDDNGMNLRNIIQDCLQLIADSDTP 180
                                                                                                                                                                                                                                                                                                                                                                  TIRKGTYTFVPWLLSFKRGNAL-------YSQVLYTDPIFAMGHVIQRKK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 VHVFGDELSLVTLFRCIQNMPKTLPNNSCYSAGIARLEEGDEIQLAIPRENAQISRNGDD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dermatological; neuroprotective; nootropic; immunomodulator; metabolic; antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever; antiparkinsonian; antipaoriatic; vasotropic; antibacterial; asthma; AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor; mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder; rheumatoid arthritis; graft-versus-host disease; immune disorder; rheumatoid arthritis; graft-versus-host disease; Crohn's disease; pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease; diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia; multiple sclerosis; Parkinson's disease; transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                              181 TIRKGTYTFVPWLLSFKRGNALEEKENKIVVRQTGYPFIYSQVLYTDPIFAMGHVIQRKK
                                                                                                                          GHRNRRAFPGPEETEQDVDLSAPPA-------LRNIIQDCLQLIADSDTP
                                                                                                                                                                                    44 SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAA-----KLLTPAAPRPHNSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;
                                                                                              1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPITPQKEEGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU10943 standard; Protein; 309 AA.
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         91.78;
                                74.48;
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                                                     230; Conservative
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TFFGALKLL 309
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                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boyle WJ, Hsu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse AGP-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU10943;
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           Query Match
                                Best Local
Matches 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a new antibody, or portion, that specifically binds to a protein which has a 285 or 250 amino acid sequence as fully defined in the specification. The antibody of the invention is useful in treating a disease or disorder such as cancer, especially B-cell cancer, autoimmune diseases such as Sjogre's carporate in the specification. The antibodie and cancer, autoimmune diseases such as Sjogre's syndrome, systemic lupus erythemateous, rheumatoid arthritis, chronic lymphocytic leukaemia, multiple myeloma, Hodgkin's lymphoma, non-Hodgkin's lymphoma or hypergammaglobulinemia, or in diagnosing a con-Hodgkin's lymphoma or hypergammaglobulinemia, or in diagnosing a cand APRIL (a proliferation-inducing ligand) in cells or body fluids using antibodies and comparing the Neutrokine-alpha and APRIL expression level with a standard Neutrokine-alpha and APRIL expression level increase or decrease in the assayed Neutrokine-alpha and APRIL expression level increase or decrease in the assayed Neutrokine-alpha and APRIL expression level disorder. The present anno acid sequence represents the mouse
Mouse; Neutrokine-alpha-like; antibody; immunogen; B-cell cancer; autoimmune disease; Sjogre's syndrome; systemic lupus erythematosus; rheumatoid arthritis; chronic lymphocytic leukaemia; multiple myeloma; Hodgkin's lymphoma; non-Hodgkin's lymphoma; hypergammaglobulinemia; APRIL; a proliferation-inducing ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    An isolated antibody or portion that specifically binds to a protein useful in the treatment of diseases such as hypergammaglobulinemia and
                                                                                                                                                                                                                                                                                                                                                             Mouse Neutrokine-alpha-like protein fragment #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ullrich S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 476-477; 482pp; English.
                                                                                                                                                                                                                              AAU79147 standard; Protein; 309 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-227008P.
2000US-234338P.
2000US-240806P.
2000US-25020P.
2001US-276248P.
2001US-293499P.
2001US-296122P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JUL-2001; 2001US-304809P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-AUG-2001; 2001WO-US25549
                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                     224 TFFGALKLL 232
                                                                                                     301 TFFGALKLL 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAR-2001;
25-MAY-2001;
07-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ebner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-MAR-2002
                                                                                                                                                                                                                                                                        AAU79147;
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Composition, useful for identifying modulator of receptor for treating asthma and glomerulonephritis, comprises AGP-3 (tumour necrosis factor ligand family member) receptor and encoding nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2; 124pp; English
12-FEB-2001; 2001WO-US04568.
                                                                             11-FEB-2000; 2000US-181800P.
                                                                                                                                                                                                                                                                                                                  WPI; 2002-049441/06.
N-PSDB; AAS18545.
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Neutrokine-alpha-like protein fragment #1

309

Sequence

cancer

Yu G,

inflammatory disorder; immune disorder; rheumatoid arthritis;

lupus and graft versus host disease.

ds sny

Domain Region Domain

/note= "intracellular domain"

cocation/Qualifiers

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The invention relates to a composition (1) comprising AGP-3 receptor attached to a vehicle protein. (1) is useful for modulating AGP-3-related activity in mesonteric lymph nodes (MiN) of a mammal. (11) is useful in assays to identify cells and tissues that express AGP-3R or proteins related to AGP-3R-related protein and for identifying compounds (agonists or antagonists) that interact with AGP-3R proteins. (11) is also useful for identifying intracellular proteins that interact with AGP-3R proteins. (11) is also useful for identifying intracellular proteins that interact with process. (11) is involved in B cell growth, survival and activation particularly in lymph node, spleen, and Peyer's patches. AGP-3R caponists and are used to treat diseases characterised by inflammatory processes or deregulated immune response such as cells mich are derived from B cells, which involves treating the hybridoma cells with (11). (11) is useful in the production of hybridoma cells with (11). (11) is useful in the treatment of inflammatory conditions of joines, e.g., rheumatoid arthritis, osteoarthritis, etc. (11), its agonises or antagonises are useful for treating acute conditions of joines, e.g., rheumatoid arthritis, osteoarthritis, etc. (11), its agonises or antagonises are useful for treating acute (11), its agonises or antagonises are useful for treating acute (11), its alonises or antagonises are useful for treating acute (11), its alonises or antagonises are useful for treating acute (11), its alonises or antagonises are useful for treating acute (11), its alonises or antagonises are useful for treating acute (11), its alonises or antagonises are useful for treating acute (11), its alonises or antagonises are useful for treating acute (11), its alonises or antagonises are useful for treating acute (11), its alonises or antagonises are useful for treating acute (11), its alonises or antagonises are useful for treating acute (11), its alonises or antagonises are useful for treating acute (11), its alonises or antagonises 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                osteoporosis, Parkinson's disease, pain, reperfusion injury, septic shock, etc. The nucleic acids are also useful for developing transgenic animals expressing (II), which are useful for producing the polypeptides and for the study of in vivo biological activity. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sathma, atherosclerosis, cachexia/anorexia, diabetes, fever, glomerulonephritis, inflammatory bowel disease, ischaemic injury including cerebral ischaemia, multiple myeloma, multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23; Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence represents the amino acid sequence of mouse AGP-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.7%; Score 1103.5; DB 23; Lenguary 74.4%; Pred. No. 3.2e-116; Lindels 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPITPQKEEGA-
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Best Local Similarity
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               셤
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'note= "unspecified amino acid encoded by AAA"

'note= "Ser encoded by TTG"

'note= "Ser encoded by /note= "Arg encoded by

'note= "Glu encoded

Misc-difference 295

Misc-difference

WO200047740-A2.

17-AUG-2000

Misc-difference 2

note= "extracellular domain"

"transmembrane

74..309 /note=

Misc-difference 106

SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAAGAPELTAGVXLLTPAAPRPHNSSR 120 SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAA-----KLLTPAAPRPHNSSR 94 The present sequence encodes a murine AGP-3 polypeptide. AGP-3 is a tumour necrosis factor (TNF) ligand family member. AGP-3 is a type II transmembrane protein, and is a potent B cell stimulatory factor.

Expression of AGP-3 correlates to increases in the number of B cells and immunoglobulins produced. AGP-3 proteins, antibodies, and nucleic acids may be used to treat inflammatory and immune disorders, or rheumatoid arthritis, Crohn's disease, lupus and graft versus host disease. The nucleic acids may be used to regulate the expression of an AGP-3 related protein. The AGP-3 proteins, antibodies and nucleic and are also useful for the detection of AGP-3 agonists, antagonists and characterizing interactions with AGP-3 related proteins.

note: this sequence is not specifically claimed. It is only mentioned in the claims, in that a polypeptide that does not comprise the present 1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPITPQKEEGAWFGICRDGRLLAATLLLALLSS Gaps 17; 21; Length 309; Score 1097.5; DB 21 Pred. No. 1.6e-115; 0; Mismatches 3; Claim 4; Fig 2; 71pp; English. 91.28; 74.18; Best Local Similarity 74.1 Matches 229; Conservative sequence is claimed. Similarity 309 AA; Sequence Query Match ઠે 셤 g ò 223 TIRKGTYTFVPWLLSFKRGNALEEKENKIVVRQTGYFFIYSOVLYTDPIFAMGHVIQRKK 240 241 VHVFGDELSLVTLFRCIQNMPKTLPNNSCYLAGIARLEEGDEIQLAIPRENAQISRNGDD 300

-----LEEGDEIQLAIPRENAQISRNGDD

VHVFGDELSLVTLFRCIQN-

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181 181 TFFGALKLL 232 301 TFFGALKLL 309

224

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Novel polypeptides comprising tumour necrosis factor ligand family proteins, useful for treating inflammatory and immune disorders, e.g.

rheumatoid arthritis

WPI; 2000-558217/51.

N-PSDB; AAA63942.

99US-0166271

(AMGE-) AMGEN INC

Boyle WJ, Hsu H;

99US-0119906

12-FEB-1999; 18-NOV-1999;

11-FEB-2000; 2000WO-US03653

AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease; type II transmembrane protein; B cell stimulatory factor;

Amino acid sequence of a murine AGP-3 polypeptide,

04-DEC-2000

XXXEXEXEX

AAB08262;

AAB08262 standard; Protein; 309 AA.

RESULT 8

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This invention describes isolated Tumor Necrosis Factor (TNF) family receptor polypeptides: APD4, APD6, APD8 and APD9 or their active fragments, and isolated TNF related ligands in and 3 (TNRL1 and TNRL3) or their active fragments. APD4 is useful for diagnosing prostate cancer by determining levels of APD4 in an individual. Prostate cancer can also be treated using APD4 selective binding agents linked to a therapeutic moiety. APD4 polypeptides are also useful for identifying selective binding agents, useful in diagnosis/treatment of disease by binding of agents to the polypeptides/active fragment which is extracellular, or expressed on the cell surface. The binding is preferably performed in vivo. APD4 polypeptides/ active fragments are also useful for screening for agonists and antagonists by binding and observing the changer in APD4 crivity. Effective pharmacological agents useful in diagnosis or treatment of disease are also identified using APD4 polypeptides/active fragments and APD4 signal transducer molecules that specifically interact with a cytoplasmic domain of APD4 and detecting a change in level of APD4 are all useful as immunogens for preparing antibodies. APD4 is also
Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4; developmental abnormality; gestational abnormalitity; prostate cancer; APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease; cytoplasmic domain; immunogen; antibody preparation; breast carcinoma; apoptosis; mouse; TNRL1-alpha.
                                                                                                            -----YSQVLYTDPIFAMGHVIQRKKVHVFGDELSLVTLFRCI 197
                                                                         GHRNRRAFQGPEETEQDVDLSAPPA--PCLPGCRHSQHDDNGMNLRNRTYTFVPWLLSFK
                                                GHRNRRAFPGPEETEQDVDLSAPPALRNIIQDCLQLIADSDTPTIRKGTYTFVPWLLSFK
                                                                                                                              New Tumor Necrosis Factor family receptor polypeptides and ligands useful for diagnosis and treatment of prostate cancer and developmental or gestational abnormalities
                                                                                                                                                                         QN------LEEGDEIQLAIPRENAQISRNGDDTFFGALKLL 232
                                                                                                                                                                                           AAW93587 standard; Protein; 290 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0924634.
                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                               Mouse TNRL1-alpha protein.
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                                                                                                            RGNAL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chaudhary PM;
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                                                                                                                                                                         198
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                                       GHRNRRAFYGGPEETEQDVDLSAPPAPCLPGCRHSQHDDNGMNLRNIIQDCLQLIADSDTP 180
                                                                                                                                                          241 VHVFGDELSLVTLFRCIQNMPKTLPNNSCYSAGIARLEEGDEIQLAIPRENAQISRNGDD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents murine Kay-ligand, which is a member of the tumour necrosis factor (TNF) family of cytokines. Pharmaceutical compositions containing the Kay-ligand can be used to suppress or stimulate the immune system, especially to prevent or reduce the severity of autoimmune diseases or response to a tissue graft or to treat cancer. An agent capable of interfering with the Kay-ligand can be used to induce cell death. The Kay-ligand can also be used to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43
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                                                                                               ---YSQVLYTDPIFAMGHVIQRKK
                                                                                                                                          -----LEEGDEIQLAIPRENAQISRNGDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human or murine Kay-ligands, members of the tumour necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Kay-ligand; tumour necrosis factor family; TNF; immune system; cytokine; autoimmune disease; tissue graft; cancer; cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 290;
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83.0%; Score 999; DB 20;
Best Local Similarity 71.9%; Pred. No. 2.1e-104;
Matches 210; Conservative 3; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPITPQKEEGA-
                                                                                                                                        VHVFGDELSLVTLFRCIQN-----
                                                                                                                                                                                                                                                                                                                 AAY04393 standard; Protein; 290 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; Page 33; 41pp; English.
                                                                              TIRKGTYTFVPWLLSFKRGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0058786.
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                                                                                                                                                                                                                           301 TFFGALKLL 309
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                                                                                                                                                                                                                                                                                                                                                                                                            Murine Kay-ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          factor family
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Kay-ligand;
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                                                                                                                                                                                                                                                                                                                               197
                                                                                                                                                                                                                                                                     CHRNRRAFPGPEETEQDVDLSAPPALRNIIQDCLQLIADSDTPTIRKGTYTFVPWLLSFK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumour necrosis factor; TNF; APBF; APRIL; BAFF; therapy; melanoma;
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ubclur for diagnosis/treatment of developmental or gestational abnormalities. APO8 was transfected to human breast carcinoma cell line MCF-7, and induced apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New heteromeric ligand of tumor necrosis factor (TNF) family, useful for diagnosis, treatment of immune system-related disorders in humans, comprises TNF-family member AFRIL subunit linked non-covalently to TNF-family member AFF subunit.
                                                                                                                                                                                                                             1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPITPQKEEGA---------VLLSS
                                                                                                                                                                       44 SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAA-----KLLTPAAPRPHNSSR
                                                                                                                                                                                                                                                                                                                               ----YSQVLYTDPIFAMGHVIQRKKVHVFGDELSLVTLFRCI
                                                                                                                            Gaps
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                                                                                                                            62;
                                                                                                Length 290;
                                                                                                                          17; Indels
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                                                                                                Score 999; DB 20;
Pred. No. 2.1e-104;
                                                                                                                          3; Mismatches
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                                                                                                83.0%;
71.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                            Matches 210; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-514644/56.
N-PSDB; AAD14418.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse BAFF protein.
                                                                                                             Local Similarity
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                                                                    290 AA;
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The present invention relates to an isolated heteromeric ligand of tumour necrosis factor (TNF)-family, referred to as APBF comprising a TNF-family member APRIL subunit linked non-covalently to TNF-family member APRIL subunit linked non-covalently to TNF-family member BAFF subunit. APBF is useful for diagnosis or treatment of various immune system-related disorders in mammals, preferably humans. Such disorders include cancer, including cellular disorders, for e.g. renal cell cancer, Kaposi's sarcoma, chronic leukaemia, breast cancer, colon cancer, bladder cancer, squamous cell carcinoma and cantoninestinal or stomach cancer, throat cancer, melanoma, colon cancer, bladder cancer, squamous cellular hyperproliferative conditions, such as scleroderma, pannus formation in rheumatoid arthritis, postsurgical scarring and lung, liver and uterine fibrosis and immunodeficiencies, inflammatory diseases, lymphadenopathy, autoimmune diseases and graft versus host disease. APBF is also useful for producing monoclonal or polyclonal antibodies and for identifying converse included and preceptors interacting converse interacting and medulators affecting bloogical function and receptors interacting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPITPQKEEGAWFGICRDGRLLAATLLLALLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAA------KLLTPAAPRPHNSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 RGNAL------YSQVLYIDPIFAMGHVIQRKKVHVFGDELSLVTLFRCI
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                                                                                                                                                                                                                                                                                                                                                                with APBF. The present sequence is mouse BAFF protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 999; DB 22;
Pred. No. 2.1e-104;
3; Mismatches 17;
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Claim 2; Fig 2d; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                83.0%;
71.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                        290 AA;
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Matches 210;
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They make the statement of the statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specifically binds to a 285 residue neutrokine-alpha protein sequence or a 250 residue APRIL (proliferation inducing ligand) polypeptide sequence (S2). Also included are: (1) an antibody or its portion that competitively inhibits the specific binding of (1) by at least 50 or 90 %; (2) a nucleic acid encoding the antibody (1) (or its single chain); (3) a vector comprising the nucleic acid, (4) a host cell comprising the nucleic acid, (4) a host cell comprising the nucleic acid or vector; and (5) a hybridoma producing the antibody. The antibody is useful for treating disease or disorder such as autoimmune diseases, systemic lugues erythematosus; rheumatoid arthritis, Sjogren's syndrome, cancer, preferably B cell cancer, chronic lymphocytic leukaemia, multiple myeloma, Hodgkin's lymphoma and non-Hodgkin's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated antibody (I) or its portion that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel antibody that binds to neutrokine-alpha protein, useful for diagnosing and treating diseases or disorders, such as autoimmune diseases, lupus erythematosus, rheumatoid arthritis, cancer, or an immunodeficiency -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ullrich S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 173; 203pp; English.
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                                                                                                   99US-122388P.
99US-124097P.
99US-127598P.
99US-130412P.
99US-130696P.
99US-13178P.
99US-13178P.
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99US-168624P.
99US-171108P.
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2001US-296122P
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                          2001US-0929493
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                          15-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dermatological, antiinflāmmatory; cardiant; ophthalmological; uropathic; antidabetic; antithyroid; antidepressant; hepatotropic.
chromosome 13q34. The present sequence is a non-human Neutrokine-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprises
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lymphocyte stimulator protein binding protein; BLyS; immune disease;
                                                                                                                                                                                                     SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAA------KLLTPAAPRPHNSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                allergy; proliferative disease; infectious disease; arteriosclerosis; inflammatory disorder; hypergammaglobulinaemia; blood clotting; ischaemia; graft-versus-host disease; neurodegenerative disease; immunosuppressive; nephrotropic; antirheumatic; antiarthitic; antioprotective; cytostatic; immunostimulant; antitumour; anti-HIV; antiasthmatic; antiallergic; thyromimetic; antianeemic; haemostatic;
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                              232
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                                                                                                        62;
                                                                                                                                                                                                                                                                                                                                                                                                              ONMPKTLPNNSCYSAGIARLEEGDEIOLAIPRENAQISRNGDDTFFGALKLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The treatment of various diseases e.g. rheumatoid arthritis, administering B Lymphocyte stimulator binding polypeptide
                                                                            Length 290;
                                                                                                        Indels
                                                                                                          17;
                                                                           Score 999; DB 23;
Pred. No. 2.1e-104;
3; Mismatches 17;
                                                                                                                                          1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPITPQKEEGA
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                                                                           83.0%;
71.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-SEP-2002 (first entry)
                                                                       Query Match 83.0°
Best Local Similarity 71.9
Matches 210; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beltzer JP, Potter DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-499775/53.
                                             290 AA;
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                                               Sequence
                 protein.
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lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells of haematopoietic origin; or proliferative disease; and reducing, inhibiting or stimulating immunoglobulin production, B cell proliferation and graft rejection involving administration of BLyS binding polypeptides are used in the treatment, prevention or amelioration of diseases such as immune system diseases, proliferative diseases of cells of hematopoietic origin, graft rejection, allergies, infectious diseases, arteriosclerosis, inflammatory disorders, hypergammaglobulinaemia, blood clotting disorders, ischaemia, and metrodegenerative diseases. The present sequence is a B lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiALDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SFTAMSLYQLAALQADLMVLRMELQSYRGSATPAAAGAPELTAGVKLLTPAAPRPHNSSR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----YSQVLYTDPIFAMGHVIQRKKVHVFGDELSLVTLFRCI 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 SFTAMSLYQLAALQADIMNIRMELQSYRGSATPAAA-----KILITPAAPRPHNSSR
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179 RGNALEEKENKIVVRQTGYFFIYSQVLYTDPIFAMGHVIQRKKVHVFGDELSLVTLFRCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 999; DB 23;
Pred. No. 2.1e-104;
3; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
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CAMBRIDGE ANTIBODY TECHNOLOGY.
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Best Local Similarity 71.9%;
Matches 210; Conservative
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16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
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(CAMB-)
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ABP ABP
AX ABP
AX ABP
AX ABP
AX ABP
AX BLy
XX KW BLy
XX KW IIIM
XW IIIM
XW IIIM
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XX COM
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Limpulcate Standlator (BLyS) polygeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell tumour necrosis factor (TNF) super family and induces B cell tumour necrosis factor (TNF) super family and induces B cell tumour necrosis factor (TNF) super family and induces B cell tumour necrosis factor (TNF) super family and induces B cell tumour neutron and differentiation. The antibodies of the irrention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABPA3990-ABPA7228 represent
                                                                                                                                                             This invention describes novel antibodies that immunospecifically bind to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GHRNRRAFPGPEETEQDVDLSAPPALRNIIQDCLQLIADSDTPTIRKGTYTFVPWLLSFK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GHRNKRAFQGPESTBQDVDLSAPPA--PCLPGCRHSQHDDNGMNLRNRTYTFVPWLLSFK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B Lymphocyte Stimulator protein; B Lymphocyte Stimulator binding peptide; BLyS; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid; synovial fluid; saliva; mucus; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAA-----KLLTPAAPRPHNSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 RGNALEBKENKIVVRQTGYFFIYSQVLYTDPIFAMGHVIQRKKVHVFGDELSLVTLFRCI
                                                                   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QN------LEEGDEIQLAIPRENAQISRNGDDTFFGALKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 999; DB 23;
Pred. No. 2.1e-104;
3; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine B Lymphocyte Stimulator (BLyS) protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPITPQKEEGA-
Vaughan T,
                                                                                                                           Disclosure; Page 3141-3142; 3148pp; English
Choi GH,
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71.9%;
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Ruben SM, . Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sest Local Similarity
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The invention relates to a B Lymphocyte Stimulator (BLyS) binding polypeptide. BLyS binding peptides bind BLyS or BLyS-like proteins reversibly. The binding peptides are used in detection, isolation and/or purification of BLyS in a solution such as water or a buffer solution, as wail as any fluid and/or cell obtained from an individual biological fluid, body tissue, body cell, cell line, tissue outlure or other source containing BLyS or BLyS-like polypeptides. The biological fluids include sera, plasma, lymph, blood, blood fraction, urine, synovial fluid, spinal fluid, saliva and muccuus. Sequences ABG33578 and ABG33579 represent murine B Lymphocyte Stimulator proteins.
                                                                                                                                                                                                                                                                                                                                                                                             New B-lymphocyte stimulator binding polypeptide useful in detecting or isolating BLyS or BLyS-like polypeptide comprises a specified amino acid sequence.
                                                                                                                                                                                                                                          Ladner RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 188-189; 269pp; English
                                                                                                                                                                                                                                      Fleming TJ,
17-AUG-2001; 2001WO-US25891.
                                                                           18-AUG-2000; 2000US-226489P
                                                                                                                                                                                                                                          Potter MD,
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                                                                                                                                                                                                                                          Beltzer JP,
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CHRNRRAFPGPEETEQDVDLSAPPALRNIIQDCLQLIADSDTPTIRKGTYTFVPWLLSFK 154 121 GHRNRRAFOGPEETEQDVDLSAPPA--PCLPGCRHSQHDDNGMNLRNRTYTFVPWLLSFK 178 -----YSQVLYTDPIFAMGHVIQRKKVHVFGDELSLVTLFRCI 197 1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPITPQKEEGAWFGICRDGRLLAATLLLALLSS 60 179 KGNALBEKENKIVVRQTGYFFIYSQVLYIDPIFAMGHVIQRKKVHVFGBELSLVTLFRCI Gaps ---LEEGDEIQLAIPRENAQISRNGDDTFFGALKLL 232 62; Length 290; Indels Score 999; DB 23; Pred. No. 2.1e-104; 3; Mismatches 17; 1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPITPQKEEGA-SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAA---83.0%; 71.9%; Query Match 83.0 Best Local Similarity 71.9 Matches 210; Conservative 155 RGNAL--------NO 44 95 198 원 ... 장. g d ò ò ద ò

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3, 2004, 07:48:17 Search completed: February Job time : 39.6667 secs

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Sequence 3233, Ap Sequence 178, App Sequence 178, App Sequence 3235, Ap Sequence 180, App Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli

Sequence:

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Sequence 2, Sequence 2, Sequence 4,

Sequence 3228, Ap Sequence 173, App

Sequence 24,

Sequence

Sequence Sequence Sequence

Appli

Sequence 1, Appli Sequence 1, Appl

Sequence 177, Sequence 177, Sequence 3234, Sequence 179, Sequence 179,

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1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPITPQKEEGAVLLSSSFTAMSLYQLAALQADL
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APPLICANT: BROYNING.
APPLICANT: BROYNING.
APPLICANT: BROWNING, Jeffrey
APPLICANT: BROWNING, Jeffrey
APPLICANT: AMBROSE, Christine
APPLICANT: TSCHOOP, Jurg
APPLICANT: SCHNEIDER, Pascal
TITLE OF INVENTION: BAFF, Inhibitors Thereof and Their Use
TITLE OF INVENTION: In the Modulation of B-Cell Response
TITLE APPLICANT: SCHNEIDER, SOUL-07-24
TITLE APPLICATION NUMBER: US/09/911,777
CURRENT APPLICATION NUMBER: 60/117,169
PRIOR PILING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: 60/143,228
PRIOR PILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 2000-01-25
NUMBER: OF SEQ ID NOS: 22
NUMBER: PSELSEQ for Windows Version 4.0
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; Pred. No. 6.4e-120;
0; Mismatches 0;
2 US-10-270-487-38

1 US-09-880-748-3232

1 US-09-932-613-177

1 US-09-932-323-177

1 US-09-932-613-179

1 US-09-932-613-179

1 US-09-911-777-1

5 US-09-911-777-1

5 US-09-912-613-178

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1 US-09-193-663-2

US-09-193-663-2

US-09-193-663-2

US-09-193-663-4

1 US-09-193-683-4

1 US-09-80-148-3228

1 US-09-877-156-1

1 US-09-133-663-4

1 US-09-133-663-4

1 US-09-133-613-133

2 US-01-137-156-1

1 US-09-133-613-2

1 US-09-133-613-3

2 US-01-137-156-1

1 US-09-133-613-328

1 US-09-133-613-328

1 US-09-133-613-328

1 US-09-137-90-18-24
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Patent No. US20020037852A1
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US-09-911-777-2
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Sequence 176, App
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                                                                                                                                                    February 3, 2004, 07:45:42; Search time 224.782 Seconds (without alignments) 216.106 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 17
Sequence 39
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1 MDESAKTLPPPCLCFCSEKG.......ENAQISRNGDDTFFGALKLL 232
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(cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
(cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
(cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
(cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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                             GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-529-93-39

US-09-880-748-330

US-09-932-613-175

US-09-932-613-175

US-09-932-487-39

US-09-929-493-40

US-09-929-493-40

US-09-923-613-176

US-09-932-613-176

US-10-270-487-40

US-09-932-613-176

US-10-214-065-8

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US-09-929-493-38
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Maximum Match 100%
Listing first 45 summaries
                                                                                                             protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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APPLICANT: MACKAY, Fabienne
RAPLICANT: KALLED, Susan
FITTE OF INVENTION: BAFF, Inhibitors Thereof and Their Use
TITLE OF INVENTION: in the Modulation of B-Cell Response and Treatment of
TITLE OF INVENTION: autoimmune Disorders
FILE OF INVENTION NUMBER: 60/117,169
PRIOR FILING DATE: 1999-01-25
PRIOR FILING DATE: 1999-01-25
PRIOR PELING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2010-01-25
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MNLRMELQSYRGSATPAAAKLLTPAAPRPHNSSRGHRNRRAFPGPEETEQDVDLSAPPAL 120
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100.0%; Pred. No. 6.4e-120.
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10045574A Publication No. US20030095967A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 232; Conservative
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; ORGANISM: Murine
US-10-045-574A-2
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US-10-045-574A-2
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US-09-929-493-39
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Sequence 39, Application US/09929493
Fatent No. US20020115112A1
GENERAL INFORMATION:
APPLICANT: Yu et al.
TITLE OF INVENTION:
FILE REFERENCE: PF343P4
CURRENT APPLICATION NUMBER: US/09/929,493

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----YSQVLYTDPIFAMGHVIQRKK 180
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Pred. No. 4.9e-109;
0; Mismatches 2;
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APPLICANT: BOYLE, WILLIAM
TITLE OF INVENTION: RECEPTOR FROM TWF FAMILY
FILE REFERENCE: A-5708
CURRENT APPLICATION NUMBER: US/09/779,050A
CURRENT APPLICATION NUMBER: 06/181,800
PRIOR APPLICATION NUMBER: 60/181,800
PRIOR FILLING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATENTIN VEYSION 3.0
SEQ ID NO 4
LENGTH: 309
PRIOR APPLICATION NUMBER: 60/225, 628
PRIOR FILING DATE: 2000-08-15
PRIOR FILING DATE: 2000-08-15
PRIOR FILING DATE: 2000-08-23
PRIOR PRIOR DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/240, 806
PRIOR APPLICATION NUMBER: 60/240, 806
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/240, 806
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-10-7
PRIOR APPLICATION NUMBER: 60/294, 499
PRIOR PILING DATE: 2001-03-06
PRIOR APPLICATION NUMBER: 60/296, 122
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 39
SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 4, Application US/09779050A; Patent No. US20020160416A1; GENERAL INFORMATION:
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Best Local Similarity 74.4*
Matches 230; Conservative
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301 TFFGALKLL 309
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CORGANISM: Mus Musculus
US-09-929-493-39
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US-09-779-050A-4
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--LRNIIQDCLQLIADSDTP
                 Score 1103.5; DB 13
Pred. No. 4.9e-109;
0; Mismatches 2;
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 95 GHRNRRAFPGPEETEQDVDLSAPPA
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Best Local Similarity 74.4%;
Matches 230; Conservative
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301 TFFGALKLL 309
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ORGANISM: mouse
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SEQUENCE 3230, Application US/09880748

PUBLICATION NO. US20030059937A1

GENERAL INFORMATION:

APPLICATON NO. US20030059937A1

FILIE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-61-17

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR PLING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR PRILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

WUMBER OF SEQ ID NOS: 3239

SEQ ID NOS: 3230

SEQ ID NOS: 3230
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                                                            DB 10; Length 309;
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Pred. No. 4.9e-109;
0; Mismatches 2;
                                                            Score 1103.5; DB 1-
Pred. No. 4.9e-109;
0; Mismatches 2;
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74.4%;
                                                            Query Match
Best Local Similarity 74.4%;
Matches 230; Conservative
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Matches 230; Conservative
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                 ORGANISM: Mus musculus
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Best Local Similarity
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    ; TYPE: PKT
; ORGANISM: Mus
US-09-779-050A-4
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 TYPE: PRT
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137 241 VHVFGDELSLVTLFRCIQNMPKTLPNNSCYSAGIARLEEGDEIQLAIPRENAQISRNGDD 300 9 94 ------YSQVLYTDPIFAMGHVIQRKK --YSQVLYTDPIFAMGHVIQRKK 44 SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAA-----KLLTPAAPRPHNSSR Gaps Sequence 175, Application US/09932613
; Sequence 175, Application US/09932613
; Publication No. US20030091565A1
; GREERAL INFORMATION:
 APPLICANT: Human Genome Sciences, Inc.
 APPLICANT: Beltzer, James P.
 APPLICANT: Petering, Tony J.
 APPLICANT: Rosen, Craig A.
 TITLE OF INVENTION: BINNING POLYPEPTIDES AND METHODS BASED THEREON
 FILE REFERENCE: Dyx-025.1 PCT; DYX-025.1 US
 CURRENT APPLICATION NUMBER: 2001-08-17
 NUMBER OF SEQ ID NOS: 458
 SOFTWARE: Patentin version 3.1
 SEQ ID NOS: 458 DB 11; Length 309; US-10-270-487-39 ; Sequence 39, Application US/10270487 ; Publication No. US20030175208A1 ; GENERAL INFORMATION:

77; Gaps

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TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLyS) FILE REFERENCE: Dyx-018.1 PCT, DYX-018.1 US
CURRENT APPLICATION NUMBER: US/09/932,322
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: Patentin version 3.1
SEQ ID NO 175
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TITLE OF INVENTION: Neutrokine-alpha and Neutrokine-alpha Splice Variant
FILE REFERENCE: PF343P4
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Pred. No. 4.9e-109;
0; Mismatches 2;
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CURRENT APPLICATION NUMBER: US/09/929,493
CURRENT FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: 60/225,628
PRIOR FILING DATE: 2000-08-15
PRIOR PLILING DATE: 2000-08-23
PRIOR PILING DATE: 2000-08-23
PRIOR PILING DATE: 2000-09-22
PRIOR PILING DATE: 2000-09-22
PRIOR PLING DATE: 2000-10-17
PRIOR PLING DATE: 2000-11-30
PRIOR PLING DATE: 2000-11-30
PRIOR PLING DATE: 2000-11-30
PRIOR PLING DATE: 2001-05-66
PRIOR PLING DATE: 2001-05-66
PRIOR PLING DATE: 2001-05-66
PRIOR PLING DATE: 2001-05-66
PRIOR PLING DATE: 2001-05-25
PRIOR PELING DATE: 2001-05-75
PRIOR PELING DATE: 2001-05-75
PRIOR PELING DATE: 2001-07-13
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, Sequence 40, Application US/09929493
, Patent No. US20020115112A1
, GENERAL INFORMATION:
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Best Local Similarity 74.4%;
Matches 230; Conservative
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SEQ ID NO 40
LENGTH: 290
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TFFGALKLL 309
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                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: mouse
                                                                                                                                                                                                                                                                                                                      US-09-932-322-175
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                            FILE REFERENCE: PR343P5
CURRENT APPLICATION NUMBER: US/10/270,487
CURRENT APPLICATION NUMBER: US/10/270,487
CURRENT PILING DATE: 2002-10-16
PRIOR PILING DATE: 2002-010
PRIOR PILING DATE: 2002-01
PRIOR PILING DATE: 2001-12-07
PRIOR PILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-10-17
PRIOR PILING DATE: 2001-10-18
PRIOR PILING DATE: 2001-10-18
PRIOR PILING DATE: 2001-10-18
PRIOR PILING DATE: 2001-10-18
PRIOR PILING DATE: 2001-10-19
PRIOR PILING DATE: 2001-0-17
PRIOR PILING DATE: 2001-08-15
PRIOR PILING DATE: 2000-08-15
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Best Local Similarity 74.4%; Pred. No. 4.9e-109;
Matches 230; Conservative 0; Mismatches 2; Indels 77; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - See File Wrapper or PALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GHRNRRAFPGPEETEQDVDLSAPPA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 57 SOFTWARE: Patentin Ver. 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIRKGTYTFVPWLLSFKRGNAL-----
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; Publication No. US20030194743A1
; GENERAL INFORMATION:
; APPLICANT: Dyax Corp.
; APPLICANT: Beltzer, James P.
; APPLICANT: Petter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Ladner, Robert Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VHVFGDELSLVTLFRCIQN-----
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TFFGALKLL 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CRGANISM: Mus musculus
US-10-270-487-39
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US-09-932-322-175
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95 GHRNRRAFPGPEETEQDVDLSAPPALRNIIQDCLQLIADSDTPTIRKGTYTFVPWLLSFK 154
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  ---YSQVLYTDPIFAMGHVIQRKKVHVFGDELSLVTLFRCI 197
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TITLE OF INVENTION: Neutrokine-alpha and Neutrokine-alpha Splice Variant
FILE REFERENCE: PF343P5
CURRENT APPLICATION NUMBER: US/10/270,487

CURRENT FILING DATE: 2002-10-16

PRIOR PLICATION NUMBER: 60/388,548

PRIOR PLICATION NUMBER: 60/336,726

PRIOR PLICATION NUMBER: 60/336,726

PRIOR APPLICATION NUMBER: 60/331,478

PRIOR APPLICATION NUMBER: 60/331,478

PRIOR FILING DATE: 2001-11-16

PRIOR PLING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/331,478
                                               179 RGNALEEKENKIVVRQTGYFFIÝSQVLYTDPIFAMGHVIQRKKVHVFGDELSLVTLFRCI
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                                                                                                                               239 ONMPKTLPNNSCYSAGIARLEEGDEIQLAIPRENAQISRNGDDTFFGALKLL 290
                                                                                                                                                                                                                                                                                                                               APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Human Genome P.
APPLICANT: Potter, M. Daniel
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Potting Polymerrides AND METHODS BASED THEREON FILE REFERENCE: Dyx-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --LEEGDEIQLAIPRENAQISRNGDDTFFGALKLL 232
                                                                                                     --LEEGDEIQLAIPRENAQISRNGDDTFFGALKLL
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Pred. No. 6.2e-98;
3; Mismatches 17;
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                                                                                                                                                                                                                                                                            Sequence 176, Application US/09932613 Publication No. US20030091565A1 GENERAL INFORMATION:
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Best Local Similarity 71.9%;
Matches 210; Conservative
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CRGANISM: mouse
US-09-932-613-176
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US-09-932-613-176
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155
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                                                                                                                                                                                                                                               1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPITPQKEEGAWFGICRDGRLLAATLLLALLSS 60
                                                                                                                                                                                                                                                                                                    44 SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAA------KLLTPAAPRPHNSSR 94
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Publication No. US2003005937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR PLING DATE: 2000-10-17

PRIOR PLING DATE: 2000-10-17

PRIOR PLING DATE: 2000-10-17

PRIOR PLING DATE: 2000-10-17

PRIOR PLING DATE: 2001-03-16

PRIOR PPLING DATE: 2001-03-25

WINDER PLING DATE: 2001-05-25
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                                                                                                                                               62;
                                                                                                  Length 290;
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6.2e-98;
                                                                                               Score 999; DB 10;
Pred. No. 6.2e-98;
3; Mismatches 17;
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83.0%; Score 999;
Best Local Similarity 71.9%; Pred. No. 6
Matches 210; Conservative 3; Mismatch
                                                                                       Query Match
Best Local Similarity 71.9%;
Matches 210; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3231
LENGTH: 290
             ) ORGANISM: Mus Musculus US-09-929-493-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Mus musculus
US-09-880-748-3231
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US-09-880-748-3231
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                                                                                                                                                                                95 GHRNRRAFPGPEETEQDVDLSAPPALRNIIQDCLQLIADSDTPTIRKGTYTFVPWLLSFK 154
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                                                                                        ----KLLTPAAPRPHNSSR
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                                        1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPITPQKEEGAWFGICRDGRLLAATLLLLALLSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BIOGEN, INC.
APPLICANT: BIOGEN, INC.
APPLICANT: Rennert, Paul D.
APPLICANT: Thomston, Useffrey S.
APPLICANT: Ambrose, Christine
APPLICANT: Ambrose, Christine
APPLICANT: Cachero, Teresa G.
TITLE OF INVENTION: Heterologous Polypeptide of the TNF
TITLE OF INVENTION: Pamily
FILE REFERENCE: A092 US
CURRENT APPLICATION NUMBER: US/10/214,065
CURRENT FILING DATE: 2002-08-07
PRIOR PILING DATE: 2000-011
PRIOR APPLICATION NUMBER: PCT/US01/04121
PRIOR FILING DATE: 2001-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                        44 SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAA----
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Pred. No. 6.2e-98;
3; Mismatches 17;
1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPITPQKEEGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/10214065 Publication No. US20030023038A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

Best Local Similarity 71.9%;
Matches 210; Conservative
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US-10-214-065-8
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| Sequence 176, Application US/0993232
| Publication No. US20030194743A1
| Publication No. US20030194743A1
| Publication No. US20030194743A1
| APPLICANT: Deter, M. Daniel | APPLICANT: Pleming, Tony J. | APPLICATION NUMBER: US/09/932,322 | CURRENT APPLICATION NUMBER: US/09/932,322 | CURRENT PILING DATE: 2001-08-17 | SOFTWARE: PatentIn version 3.1 | SOFTWARE: PatentIn version 3.1 | LENGTH: 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----YSQVLYTDPIFAMGHVIQRKKVHVFGDELSLVTLFRCI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 RGNALEEKENKIVVRQTGYFFIYSQVLYTDPIFAMGHVIQRKKVHVFGDELSLVTLFRCI 238
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Pred. No. 6.2e-98;
3; Mismatches 17; Indels
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6.2e-98;
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                PRIOR APPLICATION NUMBER: 60/329,747
PRIOR FILING DATE: 2001-10-18
PRIOR FILING DATE: 2001-10-18
PRIOR FILING DATE: 2001-10-17
PRIOR FILING DATE: 2001-08-15
PRIOR FILING DATE: 2001-08-15
PRIOR FILING DATE: 2000-08-15
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PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-09-23
PRIOR FILING DATE: 2000-09-22
PROFTWARE: PATENT APPLICATION NUMBER: 60/234,338
PRIOR FILING DATE: 2000-09-22
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Best Local Similarity 71.9%;
Matches 210; Conservative
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ORGANISM: Mus musculus
US-10-270-487-40
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ORGANISM: mouse
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PAPLICANT: Yu et al.

TITLE OF INVENTION:

TITLE OF INVENTION: Neutrokine-alpha and Neutrokine-alpha Splice Variant

TITLE OF INVENTION: Neutrokine-alpha and Neutrokine-alpha Splice Variant

CURRENT APPLICATION NUMBER: US/09/929,493

CURRENT FILING DATE: 2001-08-15

PRIOR PILING DATE: 2000-08-15

PRIOR PILING DATE: 2000-08-15

PRIOR PILING DATE: 2000-09-23

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2001-10-17

PRIOR PILING DATE: 2001-10-17

PRIOR PILING DATE: 2001-10-30-6

PRIOR PILING DATE: 2001-03-6

PRIOR PILING DATE: 2001-03-65

PRIOR PILING DATE: 2001-05-25

PRIOR PILING DATE: 2001-06-25

PRIOR PILING DATE: 2001-06-25

PRIOR PILING DATE: 2001-06-07

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---LEEGDEIQLAIPRENAQISRNGDDTFFGALKL 231
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Sequence 38, Application US/09929493
Patent No. US20020115112A1
GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 38
LENGTH: 289
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Best Local Similarity 70.1°
Matches 211; Conservative
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(c) 1993 - 2004 Compugen Ltd.
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-09-496-118B-5
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Sequence 4	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence
US-09-153-927-4	US-09-879-919-11	US-09-879-919-13	US-09-589-287B-20	US-09-588-947A-20	US-08-883-086-3	US-10-082-260-4	US-08-815-783-4	US-09-879-919-4	US-08-735-041A-2	US-09-190-476B-2	US-09-190-889A-2	US-09-190-938B-2	PCT-US95-09261-2	US-09-252-991A-18948	: US-08-471-119A-2	US-08-348-518C-4	US-08-476-509B-4
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141	141	139	125	125	125	125	125	125	91	91	91	91	91	81	78.5	77.5	77.5
28	29	30	31	33	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

61 SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAAGAPELTAGVKLLTPAAPRPHNSSR 120 288 95 GHRNRRAFPGPEETEQDVDLSAPPA---------LRNIIQDCLQLIADSDTP 137 9 94 44 SFTAMSLYQLAALQADLMNLRMELQSYRGSATPAAA-----KLLTPAAPRPHNSSR 138 -----TIRKGTYTFVPWLLSFKRGNALYSQVLYTDPIFAMGHVIQRKKVHVFGDEL 181 ALEEKENKIVVRQTGYFFI------YSQVLYTDPIFAMGHVIQRKKVHVFGDEL Gaps 81; Score 992.5; DB 4; Length 289; Pred. No. 4.1e-107; 3; Mismatches 6; Indels 81 Sequence 38, Application US/09589287B
Patent No. 6403770
GENERAL INFORMATION:
TITLE OF INVENTION: Antibodies to Neutrokine-alpha
FILE REFERENCE: PF34193C1
CURRENT APPLICATION WUMBER: US/09/589,287B
PLIOT APPLICATION AUMBER: US/09/589,287B
PLIOT APPLICATION NUMBER: 2000-06-08
PLIOT APPLICATION OF THE TEMPORE OF THE TEMPO 1 MDESAKTLPPPCLCFCSEKGEDMKVGYDPITPQKEEGA-Query Match
Best Local Similarity 70.1%;
Matches 211; Conservative TYPE: PRT
ORGANISM: Mus musculus
US-09-589-287B-38

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228
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60 CLIVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPA 119
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                                       -----TIRKGTYTFVPWLLSFKRGNALYSQVLYTDPIFAMGHVIQRKKVHVFGDEL
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Sequence 2, Application US/09589287B
Sequence 2, Application US/09589287B
Sequence 2, Application
GENERAL INFORMATION:
APPLICANT: Yu et al.
TITLE OF INVENTION: Antibodies to Neutrokine-alpha
TITLE OF INVENTION: Antibodies to Neutrokine-alpha
FILE REFERENCE: PF343P3C1
CURRENT APPLICATION NUMBER: US/09/589, 287B
Prior application data removed - check PALM or file wrapper
NUMBER OF SEQ ID NOS: 42
SOSFWARE: Patentin Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 285;
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                                                                                                                                                                                                                                                                            APPLICANT: Catherine Tribouley
TITLE OF INVERTION. NEW MEMBERS OF THE AND THER FAMILIES
TILE REPERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/286,529
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 48.7%; Pred. No. 4.5e-64;
Matches 146; Conservative 23; Mismatches 48
                                                                                                                                                                                                                                    Sequence 1, Application US/09286529
Patent No. 6297367
GENERAL INFORMATION:
                                                                181 ALEEKENKIVVROTGÝFFI----
                                                                                           SLVTLFRCIQN------
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US-09-286-529-1
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US-09-589-287B-2
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LENGTH: 285
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Pred. No. 4.1e-107;
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 Sequence 38, Application US/09588947A Patent No. 6562579
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Best Local Similarity 70.1%;
Matches 211; Conservative
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APPLICANT: Shu, Hong-Bing
APPLICANT: Shu, Hong-Bing
TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 2879-72
CURRENT APPLICATION NUMBER: US/09/565,423
CURRENT FILING DATE: 2000-05-05
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 60/132,892
PRIOR FILING DATE: 1999-05-06
60 CLTVVSFYQVAALQGDLASLRAELQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPA 119
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Sequence 23, Application US/09879919

Patent No. 6541224

GENERAL INFORMATION:

APPLICANT: Yu, Guo-Liang, et al.

TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon

FILE REFERENCE: PP253P1

CURRENT APPLICATION NUMBER: US/09/879,919

PRIOR PPLICATION NUMBER: 00/293,499

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR PILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,978

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR PILING DATE: 2001-03-16

PRIOR PELING DATE: 2001-03-16

PRIOR PELING DATE: 2001-03-16

PRIOR PLING DATE: 2000-12-13

PRIOR PLING DATE: 2000-12-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:primer
US-09-565-423-2
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120 PGEGNSSQNSRNKRAVQGPEET-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
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Matches 146; Conservative
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Patent No. 647596
GENERAL INFORMATION:
APPLICANT: Aggarwal, Bharat B.
TITLE OF INVENTION: Uses of THANK, a TNF homologue that Activates
TITLE OF INVENTION: Apoptosis
FILE REPRENCE: D6206
CURRENT APPLICATION NUBER: US/09/496,118B
                                                                                                                                                                                                                                                   83;
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                                                                                                                                                                           ; Score 622.5; DB 4;
; Pred. No. 4.5e-64;
23; Mismatches 48;
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PRIOR APPLICATION NUMBER: US 60/118,531
PRIOR FILING DATE: 1999-02-02
NUMBER OF SEQ ID NOS: 13
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Best Local Similarity 48.78
Matches 146; Conservative
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Best Local Similarity 48.73
Matches 146; Conservative
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                                              TYPE: PRT
ORGANISM: human
                                                                              7 ORGANISM: hui
US-09-589-287B-2
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APPLICANT: Yu et al.

TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokine-alpha
FILE REFERENCE: PF3418762

CURRENT APPLICATION NUMBER: US/09/588,947A

CURRENT APPLICATION NUMBER: US/09/588,947

PRIOR APPLICATION NUMBER: 09/587,968

PRIOR APPLICATION NUMBER: 09/507,968

PRIOR FILING DATE: 2000-06-08

PRIOR FILING DATE: 1999-03-02

PRIOR FILING DATE: 1999-03-12

PRIOR FILING DATE: 1999-03-12

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-04-16

PRIOR FILING DATE: 1999-04-16

PRIOR PLING DATE: 1999-04-16

PRIOR PLING DATE: 1999-04-16

PRIOR PLING DATE: 1999-04-16

PRIOR FILING DATE: 1999-04-29

PRIOR PLING DATE: 1999-04-29

PRIOR PLING DATE: 1999-04-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 VPWLLSFKRGSALEEKENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELS
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            83;
                                                                                                                                                                                                                                                                                                                                                                                         Length 285;
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/211,537
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 06/815,783
PRIOR PILING DATE: 1997-03-12
PRIOR FILING DATE: 1997-03-12
PRIOR FILING DATE: 1996-03-14
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 23
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                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-23
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TITLE OF INVENTION: Antibodies to Neutrokine-alpha
FILE REFERENCE: PF343P3C1
CURRENT APPLICATION NUMBER: US/09/589,287B
CURRENT PILING DATE: 2000-06-08
Prior application data removed - check PALM or file wrapper NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 219
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48.7%; Pred. No. 4.5e-64;
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PRIOR FILING DATE: 1996/10-25
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
PRIOR APPLICATION NUMBER: 60/167,239
PRIOR FILING DATE: 1999-11-24
PRIOR FILING DATE: 1999-11-24
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: 60/171,108
PRIOR PEDICATION NUMBER: 60/171,626
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/176,015
PRIOR APPLICATION NUMBER: 60/176,015
PRIOR PILING DATE: 1999-02-23
PRIOR PILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/036,100
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/036,100
PRIOR FILING DATE: 1998-01-12
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CORGANISM: Homo sapiens
US-09-589-287B-30
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: human
US-09-588-947A-2
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TYPE: PRT
CORGANISM: Homo sapiens
US-09-588-947A-30
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US-09-589-287B-28
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US-09-588-947A-28
                                                                                                   LENGTH: 219
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FILE REFERENCE: PF343P3C2
                                                                                                                                                              94 RGHRNRRAFPGPEETEQDVDLSAPPALRNIIQDCLQLIADSDTPTIRKGTYTFVPWLLSF 153
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                                            Gaps
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Length 219;
                                          Indels
  DB 4;
  48.4%; Score 582.5; DB 4 54.5%; Pred. No. 1.4e-59;
                                        16; Mismatches
                                                                                  51 YOLAALQADLMNLRMELQSYRGSATPAAA----
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PRIOR PELING DATE: 2000-06-08
PRIOR PELING DATE: 2000-06-08
PRIOR PELING DATE: 2000-02-22
PRIOR PELING DATE: 2000-02-22
PRIOR PELING DATE: 1099-03-02
PRIOR PELING DATE: 1999-03-12
PRIOR PELING DATE: 1999-03-12
PRIOR PELING DATE: 1999-03-16
PRIOR PELING DATE: 1999-03-26
PRIOR PELING DATE: 1999-04-02
PRIOR PELING DATE: 1999-04-16
PRIOR PELING DATE: 1999-04-29
PRIOR PELING DATE: 1999-07-06
PRIOR PELING DATE: 1999-07-06
PRIOR PELING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-07
PRIOR PELING DATE: 1999-11-24
PRIOR PELING DATE: 1999-11-24
PRIOR PELING DATE: 1999-11-24
PRIOR PELING DATE: 1999-12-03
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APPLICATION NUMBER: 60/036,100
FILING DATE: 1997-01-14
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Query Match
Best Local Similarity 54.5
Matches 127; Conservative
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61 QSSRNKRAIQGAEET-
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APPLICANT: Yu et al
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1 YQVAAVĞGDLASLRABLQGHHAEKLPARARAPKAGLGBAPAVTAGLKIFEPPAPGEGNSS
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; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokine-alpha
; FILE REFRENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFWARE: Patentin Ver. 2.1
; SEQ ID NO 28
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PRIOR APPLICATION NUMBER: PCT/US96/17957
PRIOR FILING DATE: 1996-10-25
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                           51 YQLAALQADLMNLRMELQSYRGSATPAAA-
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Matches 126; Conservative
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Best Local Similarity 54.5'
Matches 127; Conservative
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206
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ITILE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
FILE REFERENCE: PR253P1
CURRENT PAPLICATION NUMBER: US/09/879,919
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-03-23
PRIOR FILING DATE: 2001-03-23
PRIOR FILING DATE: 2001-03-6/26,875
PRIOR FILING DATE: 2000-12-16
PRIOR FILING DATE: 2000-12-16
PRIOR FILING DATE: 2000-12-13
PRIOR PRILING DATE: 2000-12-13
PRIOR PILING DATE: 2000-12-13
PRIOR FILING DATE: 2000-12-3
PRIOR FILING DATE: 2000-12-3
PRIOR FILING DATE: 2000-12-3
PRIOR PILING DATE: 2000-12-3
                                                                                                                 47; Indels 102;
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44.1%; Score 531; DB 4; Length 266;
Best Local Similarity 43.7%; Pred. No. 1.8e-53;
Matches 131; Conservative 20; Mismatches 47; Indels 1
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TITLE OF INVENTION: Antibodies to Neutrokine-alpha
FILE REFERENCE: PF34P3C1
CURRENT APPLICATION NUMBER: US/09/589,287B
CURRENT FILING DATE: 2000-06-08
Prior application.data removed - check PALM or file wrapper NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
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Patent No. 6541224
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-09-879-919-24
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                                                                          FILE OF INVENTION INTO BISECULE Methods Using Antibodies to Neutrokine-alpha FILE METANT: Yu et al. 1941972 CURRENT PAPLICANTO NUMBER: US/09/588,947A CURRENT PELICANTON NUMBER: US/09/588,947A CURRENT FILING DATE: 2000-06-08 PRICE PALICATION NUMBER: 09/588,947 PRICE PALICATION NUMBER: 09/588,947 PRICE PALICATION NUMBER: 09/588,947 PRICE PALICATION NUMBER: 09/589,947 PRICE PALICATION NUMBER: 09/507,968 PRICE PALICATION NUMBER: 06/122,388 PRICE PALICATION NUMBER: 06/122,388 PRICE PALICATION NUMBER: 06/124,097 PRICE PALICATION NUMBER: 06/13,096 PRICE PALICATION NUMBER: 06/13,096 PRICE PALICATION NUMBER: 06/13,096 PRICE PALICATION NUMBER: 06/131,096 PRICE PALICATION NUMBER: 06/131,098 PRICE PALICATION NUMBER: 06/131,096 PRICE PALICATION NUMBER: 06/131,098 PRICE PALICATION NUMBER: 
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PRIOR FILING DATE: 1996-10-25
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  Application US/09588947A
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SOFTWARE: PatentIn Ver. 2.1
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GERREAL INPOGNATION:
TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokine-alpha
FILE REPERENCE: FF34493C2
CURRENT APPLICATION NUMBER: U5/09/586,947A
CURRENT FILING DATE: 2000-06-08
PRIOR PELING DATE: 2000-06-08
PRIOR PELING DATE: 2000-06-08
PRIOR PLING DATE: 3000-02-22
PRIOR PLING DATE: 1999-03-2
PRIOR PLING DATE: 1999-03-2
PRIOR PLING DATE: 1999-03-12
PRIOR PLING DATE: 1999-03-12
PRIOR PLING DATE: 1999-03-12
PRIOR PLING DATE: 1999-03-12
PRIOR PLING DATE: 1999-04-2
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                                                                                                                                                                                                                                                                                                                                                            Length 266;
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44.1%; Score 531; DB 4;
Best Local Similarity 43.7%; Pred. No. 1.8e-53;
Matches 131; Conservative 20; Mismatches 47
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 00/815,783
PRIOR FILING DATE: 1997-03-12
PRIOR PILING DATE: 1996-03-14
PRIOR PILING DATE: 1996-03-14
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
LENGTH: 266
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US-09-879-919-24
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43.7%; Pred. No. 1.8e-53;
tive 20; Mismatches 47
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PRIOR FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: 60/167,239
PRIOR PELING DATE: 1999-11-24
PRIOR APPLICATION NUMBER: 60/168,624
PRIOR PILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: 60/171,108
PRIOR FILING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-3
PRIOR PLILOGATION NUMBER: 60/171,626
PRIOR PELING DATE: 1999-12-3
PRIOR PILING DATE: 1999-10-3
PRIOR FILING DATE: 1999-02-3
PRIOR PLILNG DATE: 1990-02-3
PRIOR PLILNG DATE: 1990-02-3
PRIOR PLILNG DATE: 1990-02-3
PRIOR PLILNG DATE: 1990-01-12
PRIOR APPLICATION NUMBER: 60/036,100
PRIOR PLILNG DATE: 1990-01-12
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Best Local Similarity 43.7%
Matches 131; Conservative
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ORGANISM: Homo sapiens
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